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**WO 03/000735 A2**

(54) Title: **NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS**

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

## NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS

## RELATED APPLICATIONS

- 5           This application claims the benefit of and priority to U.S. Provisional Application 60/301,095, filed June 26, 2001 and to U.S. Provisional Application 60/332,758, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

## 10 BACKGROUND OF THE INVENTION

- G protein-coupled receptors ("GPCRs") are a superfamily of intrinsic transmembrane cell-surface receptors that mediate the transmission of extracellular signals into the cell to produce a cellular response. There are thought to be anywhere from 400 to over 1000 different members of this family. GPCRs are
- 15   intrinsic membrane proteins, and operate by a common transduction mechanism. In their inactive state, the GPCRs bind to the G proteins. Upon activation, they stimulate guanine nucleotide exchange on the G proteins, resulting in the release of GDP and the binding of GTP. The G-protein then dissociates from the GPCR, and interacts with the adenylate cyclases, which catalyze the conversion of ATP into
- 20   cAMP. The cAMP then acts as a second messenger. The G proteins can cause intracellular coupling of the GPCRs with various intracellular enzymes, ion channels and transporters.

- GPCRs (and perforce, G proteins) are involved in an enormous range of biological processes, and have been found to regulate such processes as hydrolysis
- 25   of plasma membrane phospholipids, the  $K^+$  and  $Ca^{2+}$  ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (e.g., pituitary, adrenal, ovarian). The signal can be endogenous or exogenous or, in the case of rhodopsin receptors, the stimulus can be light. Many drugs bind to a GPCR and either produce a response or block the actions of the
- 30   normal signal. The GPCR superfamily includes the cannabinoid and opioid receptors, chemokine, histamine, angiotensin, neurotensin, vasopressin, calcitonin,

dopamine, glutamate and bombesin receptors, taste and odorant receptors, and many others.

## SUMMARY OF THE INVENTION

5           The present invention relates to human G protein-coupled receptor (GPCR) genes that are specifically odorant or olfactory receptors, particularly nucleic acids comprising GPCR genes, and the amino acids encoded by such nucleic acids. These sequences are shown in Tables I and II. In Tables I and II, each GPCR entry lists the name (*e.g.*, "MOOSE01980"), the University of California at Santa Cruz contig  
10           designation from which the sequence was analyzed (*e.g.*, "ctg13103"), the exon locations (*e.g.*, "25879000 . . 25879025...."), followed by the amino acid sequence and the nucleic acid sequence.

          In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd  
15           numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*,  
20           cDNA molecules) encoding a GPCR polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II).

          The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a GPCR in a  
25           sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-230 (odd numbers), as shown in Tables I and II, or the complement of one of SEQ ID NOs:1-230 (odd numbers); a nucleotide sequence encoding one of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II), or a fragment or  
30           derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a GPCR polypeptide, or fragment or derivative thereof, comprising

detecting (directly or indirectly) the level of expression of the GPCR polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method  
5 for preparing a polypeptide encoded by an isolated nucleic acid molecule described herein (a GPCR polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule. The invention further provides an isolated polypeptide encoded by isolated nucleic  
10 acid molecules of the invention (*e.g.*, GPCR polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II. The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about  
15 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers), preferably about 95, 96, 97, 98 and 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a  
20 method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by GPCRs. The methods of diagnosing such a predisposition in  
25 an individual include detecting the presence of a mutation in GPCR, as well as detecting alterations in expression of a GPCR polypeptide, such as the presence of different splicing variants of GPCR polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter  
30 (*e.g.*, enhance or inhibit) the activity or expression of one or more GPCR polypeptides. For example, a cell, cellular fraction, or solution containing a GPCR polypeptide or a fragment or derivative thereof, can be contacted with an agent to be



tested, and the level of GPCR polypeptide expression or activity can be assessed. The activity or expression of more than one GPCR polypeptides can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one type of GPCR polypeptide, such as different splicing variants, and the levels of the  
5 different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides that interact with one or more GPCR polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also an GPCR polypeptide, splicing variant, or  
10 fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector  
15 under appropriate conditions allows identification of polypeptides which interact with the GPCR polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of an GPCR polypeptide.

Agents that enhance or inhibit GPCR polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or  
20 inhibiting) GPCR polypeptide expression or activity by contacting a cell containing GPCR and/or polypeptide, or by contacting the GPCR polypeptide, with an agent that enhances or inhibits expression or activity of GPCR or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents  
25 that alter activity of GPCR polypeptide. The invention further pertains to methods of treating conditions mediated by GPCRs, by administering GPCR therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of GPCR polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of GPCR  
30 polypeptide.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising odorant or  
5 olfactory receptors that are a subfamily of G protein-coupled receptors ("GPCRs"),  
and the amino acids encoded by those nucleic acids.

Odorant receptors are a large family of G-protein coupled receptors,  
typically expressed in the neurons of the olfactory epithelium. Odorant receptors are  
highly sensitive and selective, and provide a fast response through activation of G-  
10 proteins. Typically, the transmembrane regions II-VII delimit a hypervariable region  
that defines the ligand specificity.

These receptors are involved in the treatment of infections and various  
diseases and conditions, including, but not limited to, many diseases are associated  
with olfactory receptor chemosensory problems. The loss of the sense of smell and  
15 the sense of taste are the most common chemosensory complaints. A reduction in  
the ability to detect odors is known as hyposmia, distortion of normal smell,  
dysosmia and a complete loss of the ability to detect odors, anosmia. A reduction in  
the ability to taste sweet, sour, bitter and salty is known as hypogeusia, a distortion  
of normal taste, dysgeusia and a complete loss, ageusia. Abnormalities in a smell  
20 and taste function frequently accompany and even signal the existence of several  
diseases or unhealthy conditions, including obesity, diabetes, hypertension,  
malnutrition, and some degenerative diseases of the nervous system such as  
Parkinson's disease, Alzheimer's disease and Korsakoff's psychosis.

With the availability of complete genomic sequences for many organisms  
25 today, including *Homo sapiens*, it has become clear that there is a need for data  
mining techniques to extract the information in them, e.g., gene prediction programs.  
Of these, the most successful ones are those based on the comparison of known  
protein or protein-derived information, or those that use expressed sequence tags  
(ESTs) to predict gene location and structure.

30 One such algorithm is GeneWise. It bases its exon prediction on the use of  
Hidden Markov Models (HMMs) of proteins to be compared against a genomic  
sequence, so that the translation of the sequence will match the model in a similar

way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5, 1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3):405-20, 1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed. Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR data base (Horn *et al.*, *Nucleic Acids Res.* 26(1):275-9, 1998), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11):444-6, 1997), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349, 2001), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2, 1999), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305, 2000) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48, 2000). When none is available, or the sequences included in some groups are too distantly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680, 1994) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8, 1999). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October 2000 Fixed Release (and its subsequent corrections) and the April 2001 Fixed Release for Tables I and II, respectively, of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than  $10^{-8}$  that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1):44-47, 2000) using BLAST (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997).

Only approximately one third of the genes were 90% or more identical to an existing human RefSeq entry and/or mRNAs from GenBank. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to

complete the match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10):1631-42, 2000).

5           The full sequences of the olfactory GPCR genes and splice variants are shown in Tables I and II as SEQ ID NOs:1-230 (odd numbers). The amino acids encoded by these nucleic acids are shown in Tables I and II as SEQ ID NOs:1-230 (even numbers).

10           A number of the genes were found to be linked with markers known to be associated with human diseases genes. These are shown in Table III. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE genetics) are also located in the same consensus using  
15           ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction  
20           from the marker. The output is the name of the peak marker and its distance to the HMM gene.

#### NUCLEIC ACIDS OF THE INVENTION

          Accordingly, the invention pertains to isolated nucleic acid molecules  
25           comprising human GPCR genes. The term, "GPCR", as used herein, refers to an isolated nucleic acid molecule selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-230 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes GPCR polypeptide (*e.g.*, a polypeptide selected from the group shown in Tables I and II,  
30           and consisting of SEQ ID NOs:1-230 (even numbers)). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from

the group consisting of SEQ ID NOs:1-230 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids which normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (e.g., as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the

nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a  
5 vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid  
10 molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector are included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified  
15 DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with  
20 chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a GPCR polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence  
25 selected from the group consisting of SEQ ID NOs:1-230 (even numbers)), or another splicing variant of a GPCR polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a GPCR polypeptide of the present invention are also the  
30 subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a GPCR polypeptide. Such variants can be naturally-occurring,

such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a GPCR polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a GPCR gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid



sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a GPCR.

Such nucleic acid molecules can be detected and/or isolated by specific  
5 hybridization (*e.g.*, under high stringency conditions). "Specific hybridization" as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a  
10 sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may  
15 share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%, 85%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on  
20 pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*,  
25 room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be  
30 determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at

- least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*,  
5 selectively) with the most similar sequences in the sample can be determined. Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556, 1991, and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998, which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step  
10 in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize.  
15 Generally, doubling the concentration of SSC results in an increase in  $T_m$  of ~17°C.

Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

- For example, a low stringency wash can comprise washing in a solution  
20 containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X  
25 SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

- The percent identity of two nucleotide or amino acid sequences can be  
30 determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between

the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used (see, *e.g.*, <http://www.ncbi.nlm.nih.gov>). In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller *CABIOS* 4(1):11-17, 1998. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5, 1994; and FASTA described in Pearson and Lipman *Proc. Natl. Acad. Sci. USA* 85:2444-8, 1988.

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a  
5 sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs:1-230 (even numbers), or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40,  
10 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers"  
15 are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500, 1991.

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40,  
20 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs:1-230 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer  
25 comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable  
30 of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer

further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967, 1991; Eckert *et al.*, *PCR Methods and Applications* 1:17, 1991; PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560, 1989, Landegren *et al.*, *Science* 241:1077, 1988, transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874, 1990) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can be obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a

polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed.,  
5 CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs:1-230 (odd numbers) and/or  
10 the complement of one or more of SEQ ID NOs:1-230 (odd numbers), and/or a portion of one or more of SEQ ID NOs:1-230 (odd numbers), or the complement of one or more of SEQ ID NOs:1-230 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs:1-230 (even numbers), or encoding a portion of one or more of SEQ ID NOs:1-230 (even numbers), and  
15 constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the  
20 duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of  
25 an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of  
30 the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic

fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (e.g., reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-230 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs:1-230 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (e.g., an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover,

certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral  
5 vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include  
10 one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the  
15 nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology*  
20 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors  
25 as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for  
30 expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel,



*supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a  
5 recombinant expression vector of the invention has been introduced. The terms  
"host cell" and "recombinant host cell" are used interchangeably herein. It is  
understood that such terms refer not only to the particular subject cell but also to the  
progeny or potential progeny of such a cell. Because certain modifications may  
occur in succeeding generations due to either mutation or environmental influences,  
10 such progeny may not, in fact, be identical to the parent cell, but are still included  
within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic  
acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*),  
insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO)  
15 or COS cells). Other suitable host cells are known to those skilled in the art.  
Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional  
transformation or transfection techniques. As used herein, the terms  
"transformation" and "transfection" are intended to refer to a variety of  
art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*,  
20 DNA) into a host cell, including calcium phosphate or calcium chloride  
co-precipitation, DEAE-dextran-mediated transfection, lipofection, or  
electroporation. Suitable methods for transforming or transfecting host cells can be  
found in Sambrook, *et al.* (*supra*), and other laboratory manuals.  
For stable transfection of mammalian cells, it is known that, depending upon the  
25 expression vector and transfection technique used, only a small fraction of cells may  
integrate the foreign DNA into their genome. In order to identify and select these  
integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics)  
is generally introduced into the host cells along with the gene of interest. Preferred  
selectable markers include those that confer resistance to drugs, such as G418,  
30 hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker  
can be introduced into a host cell on the same vector as the nucleic acid molecule of  
the invention or can be introduced on a separate vector. Cells stably transfected

with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous GPCR gene, or an exogenous nucleic acid encoding a GPCR polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule

introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in BioTechnology* 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669.

## 15 POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by GPCRs ("GPCR polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes

preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially  
5 free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment,  
10 the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

15 In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-230 (even numbers), or a portion or polymorphic variant thereof. However, the  
20 polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic  
25 acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs:1-230 (even numbers), or  
30 polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially

homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are  
5 substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or  
10 more of SEQ ID NOs:1-230 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs:1-230 (even numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

15 To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid  
20 positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two  
25 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same  
30 functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another

amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs:1-230 (odd numbers), or a complement of

such a nucleic acid (*e.g.*, SEQ ID NOs:1-230 (even numbers), or other variants).

However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example  $\beta$ -galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*,

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

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introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

#### ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided that bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs:1-230 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs:1-230 (odd numbers), or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active

portions of immunoglobulin molecules include F(ab) and F(ab')<sub>2</sub> fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

10 Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole *et al.* (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal

antibody to a polypeptide of the invention (see, e.g., *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (e.g., a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a

polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

#### DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a GPCR gene or gene product in an individual. Diagnostic assays can be designed for assessing GPCR gene expression, or for assessing activity of GPCR polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a GPCR, or a defect in a GPCR. The invention also provides for prognostic (or predictive) assays for determining whether an individual is susceptible to a disease or condition associated with a GPCR, *e.g.*, if an individual is at risk for addiction to an opioid. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a GPCR. Another aspect of the invention pertains to assays for monitoring the

influence of agents (e.g., drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

5

## DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a GPCR, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with a GPCR.

In one embodiment of the invention, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting a polymorphism in a GPCR as described herein. The polymorphism can be a mutation in a GPCR, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a GPCR gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a GPCR can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a GPCR gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription

or translation of the gene. A GPCR gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a disease or condition associated with a GPCR, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a GPCR (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a GPCR is present, and/or to determine which splicing variant(s) encoded by the GPCR is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a GPCR or contains a nucleic acid encoding a particular splicing variant of a GPCR. The probe can be any of the nucleic acid molecules described above (e.g., the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose a susceptibility to a disease or condition associated with a GPCR, a hybridization sample is formed by contacting the test sample containing a GPCR, with at least one nucleic acid probe. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion

thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs:1-230 (odd numbers), or the complement  
5 thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs:1-230 (even numbers). Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient  
10 to allow specific hybridization of the nucleic acid probe to a GPCR. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific  
15 hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the GPCR in the test sample, then the GPCR has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used  
20 concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the GPCR, or of the presence of a particular splicing variant encoding the GPCR and is therefore diagnostic for a susceptibility to a disease or condition associated with a GPCR. In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are  
25 used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition associated with a GPCR. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid  
30 probe, as described above, to RNA from the individual is indicative of a polymorphism in a GPCR, or of the presence of a particular splicing variant encoded

by a GPCR, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

5           Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate*  
10   *Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR. Hybridization of the PNA probe to a GPCR is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

15           In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a GPCR (and,  
20   if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the GPCR, and therefore indicates the presence or absence of this susceptibility to a  
25   susceptibility to a disease or condition associated with a GPCR.

          Sequence analysis can also be used to detect specific polymorphisms in a GPCR. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a GPCR, or a fragment of the gene, or  
30   cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known



nucleic acid sequence of the gene, cDNA (e.g., one or more of SEQ ID NOs:1-230 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs:1-230 (even numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the GPCR indicates that the  
5 individual has a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a GPCR, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for  
10 example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a GPCR, and that contains a polymorphism associated with a susceptibility to a susceptibility to a  
15 disease or condition associated with a GPCR. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a GPCR can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR, a test sample of  
20 DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a GPCR, and its flanking sequences. The DNA containing the amplified GPCR (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the  
25 amplified GPCR is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the GPCR, and is therefore indicative of a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In another embodiment, arrays of oligonucleotide probes that are  
30 complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a GPCR. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a

plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These  
5 arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO  
10 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261, the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is  
15 hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, Published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence which includes one or more previously  
20 identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the  
25 array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

30 Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate

arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those

5 polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of

10 nucleic acid analysis can be used to detect polymorphisms in a GPCR or variants encoding by a GPCR. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al. Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. No.

15 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al. Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981));

20 heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

25 In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a GPCR can also be made by examining expression and/or composition of a GPCR polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is

30 assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a GPCR, or for the presence of a particular variant encoded by a GPCR. An alteration in expression of a polypeptide

encoded by a GPCR can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a GPCR is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant GPCR polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting a particular splicing variant encoded by that GPCR, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a GPCR in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a GPCR. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a GPCR. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a GPCR. Various means of examining expression or composition of the polypeptide encoded by a GPCR can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as

indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant GPCR, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a GPCR, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant GPCR, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR, as is the presence (or absence) of particular splicing variants encoded by the GPCR gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a GPCR in a test sample is compared with the level or amount of the polypeptide encoded by the GPCR in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the GPCR, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. Alternatively, the composition of the polypeptide encoded by a GPCR in a test sample is compared with the composition of the polypeptide encoded by the GPCR in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the

control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a  
5 susceptibility to a disease or condition associated with that GPCR.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP  
10 analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) GPCR polypeptide, means for amplification of nucleic acids comprising a GPCR, or means for analyzing the nucleic acid sequence of a GPCR or for analyzing the amino acid sequence of a GPCR polypeptide, etc.

#### 15 SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a  
20 nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs:1-230 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence  
25 of one of SEQ ID NOs:1-230 (even numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is  
30 contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a GPCR nucleic acid), and the

contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be  
5 subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described  
10 above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, binding agents, antibodies, small molecules or  
15 other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, GPCR binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which  
20 change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with GPCR binding agents (*e.g.*, G-proteins, other receptors associated with GPCRs, or other binding agents); or which alter posttranslational processing of the GPCR polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell,  
25 such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays.  
30 Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods

requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a GPCR polypeptide, a cell, cell lysate, or solution containing or expressing a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-230 (even numbers), or another splicing variant encoded by a GPCR), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of GPCR activity is assessed (*e.g.*, the level (amount) of GPCR activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the GPCR polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a GPCR polypeptide. An increase in the level of GPCR activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) GPCR activity. Similarly, a decrease in the level of GPCR activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) GPCR activity. In another embodiment, the level of activity of a GPCR polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters GPCR activity.

The present invention also relates to an assay for identifying agents which alter the expression of a GPCR gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, G-proteins, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as



well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a GPCR polypeptide (*e.g.*, a GPCR gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution  
5 can be another solution which comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of GPCR expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level  
10 and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the GPCR expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of GPCR. Enhancement of GPCR expression  
15 indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of GPCR expression indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level and/or pattern of GPCR polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that has previously been established. A level and/or  
20 pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters GPCR expression.

In another embodiment of the invention, agents which alter the expression of a GPCR gene or which otherwise interact with the nucleic acids described herein,  
25 can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the GPCR gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter  
30 gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression

of the GPCR, as indicated by its ability to alter expression of a gene that is operably linked to the GPCR gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of GPCR activity.

5 In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

10 Agents which alter the amounts of different splicing variants encoded by a GPCR (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

15 In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a GPCR binding agent. For example, a cell that expresses a compound that interacts with a GPCR (herein referred to as a "GPCR binding agent", which can be a polypeptide or other molecule that interacts with a GPCR, such as a G-protein) is contacted with a GPCR  
20 in the presence of a test agent, and the ability of the test agent to alter the interaction between the GPCR and the GPCR binding agent is determined. Alternatively, a cell lysate or a solution containing the GPCR binding agent, can be used. An agent which binds to the GPCR or the GPCR binding agent can alter the interaction by interfering with, or enhancing the ability of the GPCR to bind to, associate with, or  
25 otherwise interact with the GPCR binding agent. Determining the ability of the test agent to bind to a GPCR or a GPCR binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$  or  $^3\text{H}$ , either directly or indirectly, and the radioisotope  
30 detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label

detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent  
5 with a GPCR or a GPCR binding agent without the labeling of either the test agent, GPCR, or the GPCR binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (e.g., Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in  
10 this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a GPCR or antagonists for studying a susceptibility to a disease or condition associated with a GPCR. Drugs could be designed to regulate GPCR activation that  
15 in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more GPCR polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song  
20 (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more GPCR polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor which has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different  
25 proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (e.g., nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and  
30 also a GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially

may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or G-protein). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies which express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the GPCR polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a GPCR polypeptide, as described above.

10 In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either GPCR, the GPCR binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the  
15 polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that  
20 allows GPCR or a GPCR binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a GPCR is contacted with a test agent and the  
25 expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison.  
30 For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide

expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by  
5 methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test  
10 agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention  
15 pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a GPCR, or to alter expression of a GPCR, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described  
20 herein.

#### PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the  
25 polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-230 (even numbers)); and/or comprising other splicing variants encoded by a GPCR; and/or an agent that alters (*e.g.*, enhances or inhibits) GPCR gene expression or GPCR polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a G-protein), an agent that alters GPCR gene  
30 expression, or a GPCR binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters GPCR polypeptide

activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to  
5 water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical  
10 preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or  
15 emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium  
20 stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction  
25 can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine  
30 procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may

also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

10 For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, e.g., pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage

ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with a GPCR, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

#### METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a GPCR, using a GPCR therapeutic agent. A "GPCR therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) GPCR polypeptide activity and/or GPCR gene expression, as described herein (*e.g.*, a GPCR agonist or antagonist). GPCR therapeutic agents can alter GPCR polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional GPCR polypeptide or by upregulating the transcription or translation of the GPCR gene; by altering



posttranslational processing of the GPCR polypeptide; by altering transcription of GPCR splicing variants; or by interfering with GPCR polypeptide activity (*e.g.*, by binding to a GPCR polypeptide), or by downregulating the transcription or translation of a GPCR gene. Representative GPCR therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a GPCR polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOS:1-230 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOS:1-230 (even numbers), or fragments or derivatives thereof); polypeptides described herein (*e.g.*, one or more of SEQ ID NOS:1-230 (even numbers), and/or other splicing variants encoded by a GPCR, or fragments or derivatives thereof);

other polypeptides (*e.g.*, G-proteins); GPCR binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant GPCR polypeptide, or an antibody to a non-mutant GPCR polypeptide, or an antibody to a particular splicing variant encoded by a GPCR, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) GPCR gene expression or polypeptide activity, or that regulate transcription of GPCR splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed).

More than one GPCR therapeutic agent can be used concurrently, if desired.

A GPCR therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a GPCR. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a GPCR polypeptide in an individual. For example, a GPCR therapeutic agent can be

administered in order to upregulate or increase the expression or availability of the GPCR gene or of specific splicing variants of GPCR, or, conversely, to downregulate or decrease the expression or availability of the GPCR gene or specific splicing variants of the GPCR. Upregulation or increasing expression or availability of a native GPCR gene or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native GPCR gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The GPCR therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a GPCR polypeptide, such as one of SEQ ID NOs:1-230 (odd numbers), or a complement thereof; or another nucleic acid that encodes a GPCR polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs:1-230 (even numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a GPCR or a cDNA encoding a GPCR polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native GPCR polypeptide. If necessary, cells that have been transformed with the gene or

cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native GPCR expression and activity, or have mutant GPCR expression and activity, or have expression of a disease-associated GPCR splicing variant, can be engineered to express the GPCR polypeptide or an active fragment of the GPCR polypeptide (or a different variant of the GPCR polypeptide). In a preferred embodiment, nucleic acid encoding a GPCR polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (e.g., microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a GPCR is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the GPCR polypeptide, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA which is complementary to a portion of the mRNA and/or DNA which encodes the GPCR polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe which is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the GPCR. In one embodiment, the oligonucleotide probes are modified oligonucleotides which are resistant to endogenous nucleases, e.g.

exonucleases and/or endonucleases, thereby rendering them stable *in vivo*.

Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the GPCR. The antisense oligonucleotides bind to GPCR mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *Bio/Techniques*

6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

5           The antisense molecules are delivered to cells that express GPCR *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form  
10           complementary base pairs with the endogenous GPCR transcripts and thereby prevent translation of the GPCR mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors  
15           can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route  
20           (*e.g.*, systemically).

          Endogenous GPCR expression can also be reduced by inactivating or "knocking out" GPCR or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a  
25           mutant, non-functional GPCR (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GPCR (either the coding regions or regulatory regions of GPCR) can be used, with or without a selectable marker and/or a negative  
30

selectable marker, to transfect cells that express the GPCR *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GPCR. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above.

- 5 Alternatively, expression of non-mutant GPCRs can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional GPCR, *e.g.*, a gene having one of SEQ ID NOs:1-230 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant GPCR in the cell, as described above. In another embodiment, targeted  
10 homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a GPCR polypeptide variant that differs from that present in the cell.

- Alternatively, endogenous GPCR expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a GPCR  
15 (*i.e.*, the GPCR promoter and/or enhancers) to form triple helical structures that prevent transcription of the GPCR in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.* 6(6):569-84 (1991); Helene, C., *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)).

- Likewise, the antisense constructs described herein, by antagonizing the normal  
20 biological activity of one of the GPCR proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a GPCR mRNA or gene sequence) can be used to investigate the role of one or GPCR in  
25 developmental events, as well as the normal cellular function of the GPCRs in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

- In yet another embodiment of the invention, other GPCR therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility  
30 to a disease or condition associated with a GPCR. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic

agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

5           A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant GPCR polypeptide in conjunction with antisense therapy targeting mutant GPCR mRNA; administration of a first splicing variant encoded by a GPCR in conjunction with antisense therapy targeting a second splicing encoded by a GPCR), can also be used.

10           The teachings of all publications cited herein are incorporated herein by reference in their entirety.

          While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without  
15           departing from the scope of the invention encompassed by the appended claims.

20

Table I

5	MOOSE01980	ctg13103 25879000..25879025, 25958335..25959244
	MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIL	
	AIGSDLHLHTPMYFFLANLSFVDMGLTSSSTVTKMLVNIQTRHHTISY	
	TGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCYSTVMRPQV	
10	CALMLALCWVLTNIVALTHTFLMARLSFCVTGEIAHFFCDITPVLKLS	
	CSDTHINEMMVFVLGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGK	
	AFSTCSSHLCVVCVFYGTLFSAYLCPPSIASEEKDIAAAAMYTIVTPM	
	LNPFIYSLRNKDMKGALKRLEFKRRKKHKKW (SEQ ID NO: 2)	
	atggaaaaccaatccagcatttctgaatttttctccgaggaatatcagcgccctccagagcaacagc	
15	agtcctctctcggaattttctgtgtatgtatctgtcaccttgactgggaacctgctcatcctctggccattggct	
	ctgacctgcacctccacacccccatgtacttttctggccaacctgtctttgtgacatgggttaacgtcctcca	
	cagttaccaagatgctggtgaatatacagactcggcatcacaccatctctatacgggttgccitacgcaaatg	
	tatttcttctgtatgtttggtgatctagacagcttctctggtgcatggcgatgaccgctatgtggccatttgc	
	caccctctctgtactccacagtcatgaggcccaagctgtgccctaattgcttgattgtgctgggtcctcacc	
20	aatatcgttggcctgactcacacgttctcatggctcgggtgtccttctgtgtgactggggaaattgtcacttttc	
	tgtgacatcactcctgtcctgaagctgtcatgttctgacaccacatcaacgagatgatggtttgtcttgggag	
	gcaccgtactcatcgtcccccttttatgcattgtcacctcctacatccacattgtgccagctatcctgagggtccg	
	aaccctgtggtgggtgggcaaggccctttccacctgcagttcccacctctgcgtgtttgtgttctatgggac	
	cctcttcagtgcctacctgtgtcctccctccattgcctctgaagagaaggacattgcagcagctgcaatgtacac	
25	catagtactcccatgtgaaccctttatctatagcctaaggaacaaggacatgaagggggccctaaagagg	
	ctcttcaaaagaagaagaacacaaaaagtgg (SEQ ID NO:1)	
	MOOSE01981	ctg15907 32670285..32670410, 32712477..32713295
	MNWENESSPKEFILLGFSDRAWLQMPLFVLLISYTTTIFGNVS	
30	IMMVCILDPKLHTPMYFFLTNLSILDLCYTTTTVPHMLVNIGCNKKTI	
	SYAGCVAHLIIFLALGATECLLLAVMSFDRYVAVCRPLHYVVMNY	
	WFCLRMAAFSWLIGFGNSVLQSSLTLNMPRCGHQEVDFHFFCEVPAL	
	LKLSCADTKPIEAELEFFSVLILLIPVTLILISYGFIAQAVLKIRSAEGRQ	
	KAFGTGCGSHMIVVSLFYGTAIMYMLQPPSSTSKDWGKMFLTLFYTVI	
35	TPSLNPLIYTLRNKDMKDALKKLMRFHHKSTKI (SEQ ID NO: 4)	
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	cattctggatcccaacttcatactccatgtatttcttctcactaatctctccatcttagatctctgtataccacaa	
	ctacagtccctcatatgttgtaaatattggttgcaaaaaagaccatcagctatgctggctgtgtggccacc	
40	tcacatcttcttgccctaggtgctacagagtgtcctctctggctgttatgtccttgacagatatgtggctgttt	
	gcagacccctccactatgtatcatcatgaattattggttctgctaaggatggcagccttctcatggctcattgg	
	tttcggcaactcagtgctgcagtcttctgactcttaacatgccacgctgtggtcaccaggaagtggaccactt	
	tttctgtgaggtgcctgcacttctcaagttgcatgtgtgacacaaagcctattgaggctgagctcttctcttag	
	tgtactaatttcttaattccagtgcattgatcctcatctcctatggcttcagctcaagcagattataaaatcag	
45	gtcagcagaaggacggcaaaaagcatttgggacatgtgggtcccatgatgtgtgtccctcttttatggaa	
	cagccatttatgtatcttcaaccaccttcacacctctaaggactggggaaagatgttctcaccctctttac	
	accgtcatcactccaagctcaaccgctcatttacaccttaagaaataaggacatgaaggatgcctgaaga	
	aactgatgagatttcaccacaaatctacaaaaata (SEQ ID NO: 3)	



MOOSE01984 ctg18147 116224..116906, 166266..166527

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FSMFFPILDLLLLTVMA YDRFVAVCHPLHYMIMNPHLCGLLVFVTWLIGV  
5 MTSLLHISLMMHLIFCKDFEIPHFFCELTYILQLACSDTFLNSTLIYFMTGVLG  
VFPLLGIIFSYSRIASSIRKIMSSTEGKYKAFSTCGSHLCVVSFLFYGTGLGVYL  
SSAVTHSSQSSSMASVMYAMVTPMLNPFITYSLRNKDVKGALGRLLSRAASC  
LLR (SEQ ID NO: 6)

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MOOSE01987 ctg15944 1720461..1721241, 1821742..1821917

MASGNLTWVTEFILVGVSDDPQLPLFLVFLVLYLLTVAGNLGITL  
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25 ALQMFFFAFADAECILAAAMAYDRYAAICNPLLYTTLMSSRRVCVCFIVLA  
YFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDTQINQLLLFAL  
CSFIQTSTFVVFISYFCILTVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFM  
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SNEW (SEQ ID NO: 8)

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40 ggcagtggttttactgttgaattcccatgttaataccaataattatagtttcagaaacaaggatgtgaaaatgctctcaaaa  
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MOOSE01989 ctg15907 29556418..29557338, 29640738..29640758

MNWVNDSEIIEFILLGFSRDPWLEFPLL VVFLISYTVTIFGNLTHLVSR  
45 LDTKLHTPMYFFLTNLSLLDLCYTTCTVPQMLVNLC SIKRVISYRGCV AQLF  
IFLALGATEYLLAVMSFDRFVAICRPLHYSVIMHQRLCLQLAAASWVTGFS  
NSVWLSTLTQLPLCDPYVIDHFLCEVPALLKLSCVETTANEAELFLVSELFH  
LIPLTLILISYAFIVRAVLRIQSAEGRQKAFGTCGSHLIVVSFLYSTAVSVYLO  
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50 (SEQ ID NO: 10)

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 10 tacagccgtctctgtgtacgtgcaaccaccttgcagctccaaggaccaaggaaagatggtttctctctctatggaatc  
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MOOSE01990 ctg13517 1551578..1551604, 1690079..1690511,  
 15 1820877..1821358  
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 AGAMAHTAAMMKLSFCKSHIINHYFCDVLP LLNLSCSNTHLNELLFIAGF  
 20 NTLVPTLAVAVSYAFILYSILHRSSEGRSKAFGTCSHLMVVIFFGSITFMY  
 FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLCWKFWP  
 GQS (SEQ ID NO: 12)

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 25 ctacttgcacaccctatgtacttctctctataactgtcctctcatagatttctgctattccagtggtatcactcccaaatgc  
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MOOSE01991 ctg16359 766137..766709, 919485..919856, 942580..942609  
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 FFFVSFVNMDSLLLCVMAYDRYVAICHPLHYTARMNLCLCVQLVAGLWL  
 40 TYLHALLHTVLIAQLSFCASNIIHFFCDLNPLLQLSCSDMPLIMQLACVDT  
 LNEMEMYLASFV FVVLPLGLILVSYGHILARAVLKIRSAEGRRKAFNTCSSHV  
 AVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVK  
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 NO:13)

MOOSE01992 ctg15944 2380342..2381089, 2437225..2437421

MEDKNQTVVTEFLLGLTDHPYQKIVLFFMFLFVYLITLGGNLGMIT  
 10 LIWIDPRLHTPMYFFLRHFHLSFVDTCFSSVSPKMLTDFVVKRAISFLGCA  
 LQQWFFGFFVAADCFLLESMAFYDCYVAICNPLLYSVAMSQRLCIQLVVG  
 VIGLMNTMTHTTNAFCLPFCGPNVINPFFCDMSPLLSLVCA DTRLNKLAVFI  
 VAGAVGVFSGLTILISYTYILMAILRIRSADGRCKTFSTCSSHLTAVFISYGT  
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 15 FCKA (SEQ ID NO: 16)

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 aataagttggcagtttcatcgtggctggagctgtgggagcttcatggtctgactatcctgatttctacattatcatccta  
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 25 cgtatggtagcccttcttattatgtacatccagtgcaaccttctccctggatcctaataaagtagtctgtgtttacacag  
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MOOSE02000 ctg14877 55693..55722, 232653..233561

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 VILATNNCFLLTAMGYDRYVAICRPLRYTVIMSKGLCAQLVCGSFGIGLTM  
 AVLHVTAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEINYGVSSSFVIFVP  
 IGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSE  
 35 SSIEKDLVLSVTYTIITPLNPVVYSLRNKEVKDALCRVLCLHKIITSW (SEQ  
 ID NO: 18)

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 ccacactcccatgtatttcttctaagcatgctggctagtctagagacgggtgtacacactggctattgtgccacgaatgctttt  
 40 gagcctcatttccataaccaacctatctccttggcaggctgtgctacacaaatgttctttttgtatcttggccactaataattg  
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MOOSE02003 ctg13517 1950134..1951056, 1975668..1975683

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YFFLVFVIAECYMLTVMAYDRYVAICHPLLYNIMSHHTCLLLVAVVYAIGL  
5 IGSTIETGLMLKLPYCEHLISHYFCDILPLMKLSCSSTYDVEMTVFFSAGFNII  
VTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHLAAVGMFYGSTAFMYLK  
PSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGKLIHHRW  
(SEQ ID NO: 20)

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20 aacgctgaggggtaaacctcattcatcataggtgg (SEQ ID NO: 19)

MOOSE02005 ctg13657 1700549..1700902, 1802976..1803502,  
1973146..1973212

MESGNQSTVTEFIFTGFPQLQDAFQLLFFSIFLATYLLTLENLLILAI  
25 HSDGQLHKPMYFFLSHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQ  
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LMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSCEASQAEMMVIFFLS  
ILVLLVPLVLIFISYIFIVSTILKISSVEGQCKAFATCASHLTVVVVHYGCASFI  
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30 NSKTIV (SEQ ID NO: 22)

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MOOSE02012 ctg12559 8951547..8952461, 9093750..9093773

MGDNITSIREFLLLGFPVGPRIQMLLFGLFSLFYVFTLLNGTILGLISL  
45 DSRLHAPMYFFLSHLAVVDIAYACNTVPRMLVNLLHPAKPISFAGRMMQTF  
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LSLIHLVLLPLPFCRPQKIYHFFCEILAVLKLACADTHINENMVLAGAISGLV  
GPLSTIVVSYMCI LCAILQIQSREVQRKAFRTCFSHLCVIGLVYGTAIMYVGP  
50 RYGNPKQKKYLLLFHSLFNPMLNPLICSLRNSEVKNTLKRVLGRSQWCKS

- 64 -

## Q (SEQ ID NO: 24)

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15 MOOSE02013 ctg13103 7556019..7556060, 7752122..7753039

MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVILLGNGTLILISI  
LDPHLHTPMYFFLGNL SFLDICYTTTSIPSTLV SFLSERKTISFSGCAVQMFLG  
LAMGTTECVLLGMMAFDRYVAICNPLRYPIIMSKNAYVPM AVGSWFAGIV  
NSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGNEFLMLVATILF  
20 TLMPLLLIVISYSLISSLKIHSSSEGRSKAFSTCSAHLTVVIIIFYGTILFMYMKP  
KSKETLNSDDLDATDKIISMFGVMTPMMNPLIYSLRNKD VKEALCRLFRS  
GFHSQYN (SEQ ID NO: 26)

atggaatgggaaaaccaaacattctgtggaatttttctgaaggacattctgtcacccaaggcttgagtta  
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25 ctccacacctatgtacttcttctggggaacctctccttctggacatctgctacaccaccacctatctccctccacactag  
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gagtgtgtgcttctgggcatgatggccttggaccgtatgtggctatctgcaacctctgagatattccatcatcatgagca  
agaatgcctatgtacccatggctgttgggtcctggttgcagggttgcaactctgcagtacaaactacattttagtagtaa  
ttgccttctgcaggaagaatgtcatcaatcatttctcatgtgaaattctagctgtcatgaagtggcctgtgtgacatctcag  
30 gcaatgagttcctcatgcttggccacaataattgtcacatgatgccactgctcttgatagttatcttactattaatcatt  
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aaattatatccatgttctatggggtgatgactcccatgatgaatccttaattctacagtcttagaacaaggatgtgaagag  
gcactctgcaggctgtcaggagtggattcattccagtagcaac (SEQ ID NO: 25)

35 MOOSE02014 ctg53 48293..48490, 296652..297358, 314735..314759

NHSRVTEFVLLGLSSSRELQPFLLTFSLLYLAILLGNFLILTVTSDSR  
LHTPMYFLLANLSFIDIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGT  
TECFFLSVMAYDRYLAICRPLHYP SIMTGKFCILVCVCWVGGFLCYPVPIVL  
40 ISQLPFCGPNIDHLVCDPGLFALACISAPSTELICYTFNSMIIFGPFLSILGSYT  
LVIRAVLCIPSGAGRTKAFSTCGSHLMVVSFLFYGTLMVMYVSPTS GNPAGM  
QKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGRRQWPSSI (SEQ ID  
NO: 28)

aatcattctcgggtgacagaatttgtgtgtggtgactgtctagtccaaggagctccaacctttctgtttcttaca  
45 ttttactactttatagcaattctgttgggcaacttctcatcactcactgtgacctcagattccgccttcacacccccat  
gtacttctgcttgcacacctgtcatttatagacatctgttacatttctcactgtcccaacatgctagtcaatatcctctctg  
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50 gaccacttgggtgtgacccaggccattgttgcactggcctgcactctgtccttccactgagcttattgttacaccttc

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tgctggcgaactaaagcttctccacatgtgggtcccacctaattgggtgtctctattctatggaacccttatggatgta  
tgtgagcccaacatcagggaaccagcaggaatgcagaagatcatcactctggatacacagcaatgactccattctaa  
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ctatc (SEQ ID NO: 27)

MOOSE02016 ctg13657 2010295..2010336, 2020876..2021775  
MDTGNWSQVAEFILGPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLV  
VCLDSRLHTPMYHFVLSFSELGYTAATIPKMLANLFSEKKTISFSGCLLIQY  
10 FFHSLGATECYLLTAMAYDRYLAICRPLHYPTLMPTLCAEIAIGCWLGLA  
GPVVEISLISRLPFCGPNRIQHVFCDFFPVLSLACTDTSTNVLVDFVINSCKIL  
ATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHLTVVLFYGSILSMYVRL  
KKSYSLDYDQALAVVYSVLTPLNPFTYSLHNKEIKEAWKKYICRRQPATE  
M (SEQ ID NO: 30)

15 atggacacagggaaactggagccaggtagcagaattcatcatcttgggcttccccatctccagggtgccag  
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20 accccaacacttgtgcagagattgccattggctgtgtgggtgggaggcttggctgggcccagtagttgaaattcctgatttc  
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25 gcagtggctactcagtgctcacaccttccctcaaccttcatctacagcttcacaaacaggagatcaaggaggcttgg  
aaaaagtacatctgcaggaggcagccagccacggaaatg (SEQ ID NO: 29)

MOOSE02017 ctg14667 1151783..1151789, 1152941..1153872  
MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFIFYSLTLFGNTIIIALSWL  
30 DLRLHTPMYFFLSHLSLLDLCTTSTVPQLLINLCGVDRTTTRGGCV AQLFIY  
LALGSTECVLLVVMADFDRYA A VCRPLHYMAIMHPHLCQTLAIASWGAGFV  
NSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGTEAKMFVARVIV  
VAVPAALILGSYVHIAHA VLRVKSTAGRRKA FGTCGSHLLVFLFYGSAIYT  
YLQSIHNYSEREGKFVALFYTTITPILNPLIYTLRNKDVKGALWKVLWRGRD  
35 SGQW (SEQ ID NO: 32)

atgggaagtccaacaccagtttgaagatggctcatttgggtgggattctcagattggccgcaactggagccc  
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gcacacacctatgtacttcttctctctctgtccctcctggacctctgcttaccaccagcaccgtgccccagctcctgat  
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40 cagagtgtgtcctcctgggtgatggcctttgaccgctatgctgtgtgtgtgtcctaccactacatggccatcatgca  
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45 gtagtttctctttttaggtcagccatctacacatatctccaatccatccacaattattctgagcgtgagggaaaattgtgc  
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MOOSE02019 ctg53 1139348..1139380, 1231694..1232602

MKGANLSQGMFELLGLTTDPQLQRLLFVVFLGMYTATLLGNLVMF  
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QMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVCASLIVGSYSA  
5 GFLNSLIHTGCFISLKFCAHVVTHFFCDGPPILSLSCVDTSCEILLFIFAGFN  
LLSCTLTILISYFLILNTILKMSSAQGRFKAFTCASHLTAICLFFGTTLFMYLR  
PRSSYSLTQDRTVAVIYTVVIPVLNPLMYSLRNKDVKKALIKLLKKLFISFPD  
(SEQ ID NO: 34)

atgaaaggggcaaacctgagccaaggatggagttgagctcttgggcctcaccactgacccccagctcca  
10 gaggctgctcttctgtgtgttcctgggcatgtacacagccactctgctggggaacctgggtcatgttctctgatcatgtg  
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20 aaagcttttaagaaattgtttataagcttccagat (SEQ ID NO: 33)

MOOSE02020 ctg15944 2581969..2582449, 2606297..2606721,  
2726123..2726158

MGRGNSTEVTFFHLLGFGVQHEFQHVLFIVLLLIYVTSLIGNIGMILLI  
25 KTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEENNLITFRGCVIQL  
VYATFATSDCYLLAIMAMDCYVAICKPLRYPMMSQTVYIQLVAGSYHIGSI  
NASVHTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLI  
FTGLVVIFSYTYIMATILKMSSAGRKKSFTCASHLTAVTIFYGTLSTMYLQ  
SHSNNSENKMKVAFIFYGTVPMLNPLIYSLRNKEVKEALKRLLWSECCVSNQ  
30 N (SEQ ID NO: 36)

atgggtcagaggaaacagcactgaagtgtgaattccatcttctgggatttgggtccaacacgaatttcagca  
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acttcaaacaccatgtactttttccacaacatttggctttgtgatatctgttatacttctgtatcactccaagatgtcca  
aagcttcacagaagaaaataatttgataacatttggggctgtgtgatacaattcttagttatgcaacatttgaaccagtga  
35 ctgttacctcctagctattatggcaatggattgttattgttccatctgtaagccccctcgtatcccatgatcatgtcccaaca  
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40 acactcttcatgtatttgcagtctcatttcaataatccaggaaaatgaaagtggcctttatatttggcacagtatt  
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gtctcccaaat (SEQ ID NO: 35)

MOOSE02023 ctg15944 3691512..3691544, 3844394..3845284,  
45 3904316..3904339

MLEGNLTSVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAILV  
VGLDHRRLRRPMYFFLTHLSCLEIWTSTVTPKMLAGFIGVDGGKNISYAGC  
LSQLFIFTFLGATECFLLAAMAYDRYVAICMPLHYGAFVSWGTCIRLAAAC  
WLVGFLTPILPIYLLSQLTFCGPNVIDHFS CDASPLLALSCSDVTWKETVDFL  
50 VSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTSCAAHLTVVSLFY

GTLFFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKALGRT  
LSQKKKKKKKN (SEQ ID NO: 38)

atgtagaaggaaatctaccagcgtactgaattgtcatgatgggcttggcgcacccatgaagcacacctc  
ctctcttcatactcttctcaccatgtacctgttcaccttggaggagaattggccatcatttagtggtgggttggaccacc  
5 gactacggagaccatgtatttctctgacacacttgccttgccttgaatctggtacacttctgttacagtcccaagatg  
ctggctgggtttattgggtggatgggtgcaagaatactcttattgctggttgcctatcccagctcttcatcttcaccttcttgg  
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10 cacttggaggagactgtgatttctgtgtcttggctgtgctactggcctcctctatggcattgctgtgctcctatggcaa  
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gaactctgtctcaaaaaaaaaaaaaaaaaaaaaa (SEQ ID NO: 37)

15 MOOSE02024 ctg15285 7036487..7036516, 7045683..7046006,  
7131678..7132265

MKNRTMFGEFILLGLTNQPELQVMIFLFLTYMLSILGNLTITLTLDD  
PHLQTPMYFFLRNFSFLEISFISIFIPRFLTSMITTGNKVISFAGCLTQYFFAIFL  
20 GATEFYLLASMSYDRYVAICKPLHYLTIMSSRVCIQLVFCSWLGGFLAILPPII  
LMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMISVMTATIVFIMIPFS  
LIVTSYRILGAILAMASTQSRRKVFSTCSSHLLVSLFFGTASITYIRPQAGSS  
VTDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLPLRKWLRIW (SEQ  
ID NO: 40)

25 atgaaaaacagaacctgttggtagtttacttactgggccttacaatacaacctgaactccaagtgtatgat  
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gacccccatgtatttcttctccggaatttctctttagaaatttcttcacatcattttattcccagatttctgaccagcatg  
acaacaggaaataaagtatcagcttctgtggctgctgactcagatttttctatatttcttggagctaccgagtttacct  
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30 acaactagtgttctgctcctgttgggggattcctagcaatctaccaccaatcatcctgatgaccaggtagatttctgtg  
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35 cacagtcacacacccatgctcaacccatcatctacaccttgggaacaaggacgtgaggagggccctgcgacacttg  
ctgccttggagaaagtgggtgagaatatgg (SEQ ID NO: 39)

40

## Table II

45

MOOSE06786 ctg18433 219426..220365,  
MKSWNNTIILEFLLLGISPELQAFLEFLSMYLVTVLGNLLIILATI  
SDSHLHTPMYFFLSNLSFVDICFVSTTVPKMLVNIQTHNKVITYAGCITQMCFL  
FLLFVGLDNFLLTVMAYDRFVAICHPLHYMVIMNPQLCGLLVLASWIMSVL



NSMLQSLMVLPLPFCTHMEIPHFCEINQVVHLACSDTFLNDIVMYFAVALL  
GGGPLTGILYSYSKIVSSIRAISSAQGKYKAFSTCASHLSVVSIFYGTCLGVY  
LSSAATHNSHTGAAASVMYTVVTPMLNPFYISLRNKHKGAMKTFFRGKQN  
RKAI (SEQ ID NO: 42)

5 atgaaatcatggaacaataaatttagaatttctctcctgggaattcagaggaaccagaattgcaggcct  
tcctctttgggctgtcctgtccatgtacctggcactgtgctcgggaacctgctcatcctggccacaatctcagactcc  
cacctccacacccccatgtacttctctccaacctgtcctcgtagacatctgtttgtctctaccactgtcccgaagatgc  
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15 acactgtggtcaccctcatgtgaacccttcatctacagtctgaggataaacacataaagggtgctatgaaacattctt  
cagaggaaagcaaaatagaaggctatt (SEQ ID NO: 41)

MOOSE06791 ctg15907 32399000..32399533, 32422271..32422654,  
32470431..32470448,

20 MLNTTSVTEFLLLGVTDIQELQPFLFVFLTIYFISVAGNGAILMIVISD  
PRLHSPMYFFLGNLSCLDICYSSVTLPKMLQNFLSAHKAISFLGCISQLHFFH  
FLGSTEAMLLAVMAFDRFVAICKPLRYTVIMNPQLCTQMAITWIMIGFFHAL  
LHSLMTSRLNFCGSNRIYHFFCDIQPVLQLVCGDTSLNELQIILATALLILCPF  
GLILGSYGRILVTIFRIPSVAGRRKAFSTCSSHLIVVSLFYGTALFIYIRPKASY  
25 DPATDPLVSLFYAVVTPILNPIIYSLRNTEVKAALKRTIQKTAFFHSSW (SEQ  
ID NO: 44)

atgctgaataacaacctcagtcactgaatttctctttgggagtgacagacattcaagaactgcagcctttctctt  
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35 ccatctccggatcccatctgttgcggcgccgcaaggccttctccacctgctcctccacctgatcgtggtctcctctt  
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ccagaaaacggcatttcacagcagttgg (SEQ ID NO: 43)

40 MOOSE06792 ctg15907 32026075..32026200, 32068267..32069085,  
MNWENESSPKFILLGFSDRAWLQMPLFVLLISYTTITFGNVSIMMV  
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IIFLALGATECLLLAVMSFDRYVAVCRPLHYVVMNYWFCLRMAAFSWLIG  
FGNSVLQSSLTLNMPRCGHQEVDFHCEVPALLKLSCADTKPIEAELEFFSVL  
45 ILLIPVTLILISYGFIQAQAVLKIRSAEGRQKAFGTCGSHMIVVSLFYGTAIYMY  
LQPPSSTSKDWGKMFLTLFYTVITPSLNPLIYTLRNKDMKDALKKLMRFHH  
KSTKI (SEQ ID NO: 46)

atgaattgggaaatgagagctcccaaaagagttataactacttggtctcagatagggtggtacaaatg  
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50 aacttcatactcccatgtatttcttctcactaatctctccatcttagatctctgtataaccacaactacagtcctcatatgttgg

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atgagatttcaccacaaatctacaaaaata (SEQ ID NO: 45)

10 MOOSE06799 ctg13103 26750090..26750116, 26765948..26766852,  
26824997..26825006,

MEGMNQTTVSDFLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLIL  
AISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQL  
15 YFLLMFGGLDNCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVL  
TNCPALMHTLLLTRVAFCAQKAIPHFYCDPSALLKLACSDTHVNELMIITMG  
LLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKAFSTCGSHLTVVLLFYGSLM  
GVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALGKLFHRKF  
DSKRI (SEQ ID NO: 48)

20 atggaggggaatgaaccaaacctgtttcagacttctccttctaggaactctctgagtgccagaggagcagc  
ctcttctgtttggcatcttcttggcatgtacctggcaccatgggtgggaacctgtcattatcctggccatcagctctgacc  
cacacctcactatcccatgtacttcttctggccaacctgtcattaactgatgcctgttctacttctgcctccatccccaaat  
gctggccaacattcataccagagtcagatcatctcgtattctgggtgtcttgcacagctatatttctccttatgtttgggtggc  
cttgacaactgcctgctggtgtgtgatggcatatgaccgctatgtggccatctgccaaccactccattacagcacatctatga  
25 gtccccagctctgtgcactaatgctgggtgtgtgctgggtgctaaccaactgtcctgccctgatgcacacactgttgctgac  
ccgctggtgttctgtgccagaaagccatccctcatttctattgtatcctagtgtctcctgaagcttgctgctcagatac  
ccatgtaaacgagctgatgatcatcaccatgggcttgcgtgttcctcactgttccccctcctgctgatcgtcttctcctatgtccg  
cattttctgggtgtgttctcatctcatctcctggaggagatggaaggccttctctactgtgttctcatctcacgggtggt  
ctgctcttctatgggtctcttattgggtgtgtatttacttctccatcaacttactctacagagaggggaaagtagggctgtgttc  
30 tctatattggtgattatccacgctaaccattcatttatagcttgaggaaacagagacatgaaggaggcttgggtaaacctt  
ttcacagaaaatttgatagtaaaaggata (SEQ ID NO: 47)

MOOSE06800 ctg13103 26713968..26714879, 26718054..26718080,  
GRVNQTTVSDFLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLILAI  
35 SSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYF  
LLMFGGLDNCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLT  
NCPALMHTLLLTRVAFCAQKAIPHFYCDPSALLKLACSDTHVNELMIITMGL  
LFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKAFSTCGSHLTVVLLFYGSLMG  
VYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALGKLFCAFS  
40 FSSL (SEQ ID NO: 50)

ggcagagtgaaccaaacctgtttcagacttctccttctaggaactctctgagtgccagaggagcagcctc  
ttctgtttggcatcttcttggcatgtacctggcaccatgggtgggaacctgtcattatcctggccatcagctctgacca  
cacctccatactcccatgtacttcttctggccaacctgtcattaactgatgcctgttctacttctgcctccatccccaaatgc  
tgccaacattcataccagagtcagatcatctcgtattctgggtgtcttgcacagctatatttctccttatgtttgggtggcctt  
45 gacaactgcctgctggtgtgtgatggcatatgaccgctatgtggccatctgccaaccactccattacagcacatctatgagt  
ccccagctctgtgcactaatgctgggtgtgtgctgggtgctaaccaactgtcctgccctgatgcacacactgttgctgacc  
cgcgtggcttctgtgccagaaagccatccctcatttctattgtatcctagtgtctcctgaagcttgctgctcagatacc  
catgtaaacgagctgatgatcatcaccatgggcttgcgtgttcctcactgttccccctcctgctgatcgtcttctcctatgtccgc  
atttctgggtgtgttctcatctcatctcctggaggagatggaaggccttctactgtgttctcatctcacgggtggtc  
50 tgctctctatgggtctctatgggtgtgtatttacttctccatcaacttactctacagagaggggaaagtagggctgtgttct

ctatatggtgattattcccacgctaaccattcattatagcttgaggaaacagagacatgaaggaggcttgggtaaactttt  
ttcgagagcttttagtttctcatcatta (SEQ ID NO: 49)

MOOSE06803 ctg15907 30939074..30939994, 30982809..30982829,  
5 MNWVNDSEIIEFILLGFSRDPWLEFLLVFLISYTVTFGNLTILVSR  
LDTKLHTPMYFFLTNLSLLDLCYTTCTVPQMLVNLCSSIRKVISYRGCVAQLF  
IFLALGATEYLLLA VMSFDRFVAICRPLHYSVIMHQRLCLQLAAASWVTGFS  
NSVWLSTLTQLPLCDPYVIDHFLCEVPALLKLS CVETTANEAEFLVSELHFH  
LPLTLILISYAFIVRAVLRIQSAEGRQKAFGTCSHLLIVVSLFYSTAVSVYLQ  
10 PPSPPSKDQGKMVSLFYGLAPMLNPLIYTLRNKEVKEGFKRLVARRSFCSS  
(SEQ ID NO: 52)

atgaattgggtaaatacagcatcatcacaggagttattctgctgggttctcagatcgacctggctggagtttc  
cactcctgtggtcttctgatttctacactgtgacctcttggcaatctgacctattctagtgtcacgctggacacaaa  
cttcatacccccattgtatttttcttaccatctatcactcctggtctgttaccacacatgtacagtcacacaaatgtagta  
15 aattatgcagcatcaggaaagtaacagttatogtggctgtgtagcccagcttttcatatttctggccttgggggctactgaa  
tatcttctcctggcgtcatgtccttctgataggtttagctattgtcggcctctccattactcagttatcatgcaccagagact  
ctgctccagttggcagctgcacctgggttactggttttagtaactcagtggtgtctaccctgactctccagctgccact  
ctgtgaccttatgtgatagatcatttctctggaagtcctgcactgtcaagttatctgtgtgagacaacagcaaatga  
ggctgaactattcctgtcagtgagctcttccatctaataccctgacacitaccttatcatatgctttttatgtccgagcag  
20 tattgaggatacagctgctgaaggtcgacaaaagcattgggacatgtggttcccatctaattgtggtgtctcttttatag  
tacagccgtctgtgtacctgcaaccaccttgcacagctccaaggaccaaggaagatggttctcttctatggaatc  
attgcacccatgtgaatcccttatatacacttaggaacaaggaggtaaagggaaggctttaaagggttggtgcaaga  
cggttcttctgtcatccacc (SEQ ID NO: 51)

MOOSE06809 ctg4256 15356000..15356015, 15362637..15363562,  
25 MGLGNESSLMDFILLGFSRDPWLEFLLVFLISYTVTFGNLTILVSR  
LDPPLHTPMYFFLTNLSLLDICFTTSLAPQTLVNLRPKKTTTYGGCVAQLYI  
SLALGSTECILLADMALDRYIAVCKPLHYVIMNPRLCQQLASISWLSGLAS  
SLIHATFTLQLPLCGNHRDLHFCEVPALLKLACVDTTVNELVLFVSVLFLV  
30 VIPPALISISYGFTTQAVLRIKSVBARHKAFSTCSSHLTVVIIIFYGTIIYVYLQPS  
DSYAQDQGKFISLFYTMVTPTLNPIIYTLRNKDMKEALRKLISGKLISKQN  
(SEQ ID NO: 54)

atgggattgggcaatgagagttccctaatggattcatccttctaggcttctcagaccacccctgctgagggt  
gttctcttctgatttgccttttcttacctctgacctgtgggaaactcaccataatcatcatctcatatggtacccctc  
35 ttcataccccaatgtacttttctcagcaacctcttcttactggacatctgcttactactagccttgcctcctcagacctgta  
acttgcaagaccaaagaagacgatcacttacggtggtgtgtggcgcaactctataattctctggcactggggtccactg  
aatgtatcctcttggctgacatggccttggatcggtacattgtgtgtgcaaacccctccactatgtagtcatcatgaacca  
cggcttgcacaagctggcatctatctctggtcagtggttggctagttccctaatccatgcaactttaccttgcaattg  
cctctctgtggcaaccataggctggaccattttattgcgaagtaccagctcttctcaagttggcttgtgtggacaccactgt  
40 caatgaattggtgcttttctgttagtgttctgttctgtcattccaccagcactcatctccatctctatggctcataactcaa  
gctgtgctgaggatcaaatacagtagaggcaaggcacaagccttcagcacctgctcctccaccttacagtgggtgattat  
attctatggcaccataatctacgtgtacctgcaacctagtacagctatgccaggaccaagggaagttatctccctctct  
acaccatggtgacccccactttaaatctatcatctatacttaagggaacaaggatataaagaggctctgaggaaactct  
ctcgggaaaattgatctctaacagaat (SEQ ID NO: 53)

MOOSE06813 ctg13103 26845545..26846093, 26908345..26908738,  
45 MGRNNLTRPSEFILLGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRS  
DTRLQTPMYFFLSILSFVDICYVTVIIPKMLVNFLSETKTISYGECLTQMYFFL  
AFGNTDSYLLAAMAIDRYVAICNPFIYTTIMSHRCCVLLLVLSPHIFHSL  
50 HILLTNQLIFCASNVIHHFFCDDQPPVLKLS CSDTSSSQMVVMTETLAVIVTP

FLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFRPLS  
MYSVMKGRVATVMYTVVTPMLNPFYISLRNKDMKRGLKKLRHREFTHRK  
N (SEQ ID NO: 56)

5 atgggaagaaataacctaacaagaccctctgaattcatcctccttgactctcctcgcacctgaggatcagaa  
gccgctctttgtgtgtctcctcccatctacattatcacagttaggaacctgctatcatcctggccatccgctcagaca  
ctcgtctccagagcccaigtacttcttctaagcatcctgtctttgtgacattgctatgtgacagtcattatccctaagatg  
ctgggtgaacttcttatcagagacaaagaccatctcttacgggtgagtgtctgaccagatgtacttttcttagcctttggaac  
acagacagttacctgtagcagccatggccattgaccgctatgtggccatataatcccttccactacatcaccattatga  
gtcacagatgctgtgctcctgcttctcctctctgcatccacatttccctcctgcacatttctgactaatcagc  
10 tcatctctgtgctccaatgtcatccatcattttctgcgatgatcaaccacctgtgctaaagctcctgctctgacacatc  
ctccagccagatgggtggtgatgactgagaccttagctgtcattgtgaccccttctgtgtaccatcttctctacctgcaa  
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ggctcctgttctatgggagtgatcatctatgtctatttaggcctctgtccatgtactcagtgatgaaggccgggtagccacag  
ttatgtacacagtagtgacacccatgctgaacctttcatctacagcctgaggaacaaagatatgaaaagggtttgaaga  
15 aattaagacacagagaatttactcatagaaagaac (SEQ ID NO: 55)

MOOSE06815 ctg13517 1607901..1607927, 1667204..1668118,

MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVTVVGNLGM  
LLIAVSPLLHTPMYFLSSLSFVDFCYSSVITPKMLVNFLGKKNLILYSECMV  
20 QLFFVVFVVAEGYLLTAMAYDRYVAICSPLLYNAMSSWVCSLLVLAFF  
LGFLSALHTSMMKLSFCKSHINHYFCDVLPLLNLSCSNTHLNELLLFIA  
GFNTLVPTLAVAVSYAFILYSILHRSSEGRSKAFGTCSSHLMAVVIFFGSITF  
MYFKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLRRRR  
QPSRW (SEQ ID NO: 58)

25 atgacatggaaaattatctatggcagctcagttgtcttagatgggttaacacagcaagcagagctccagctg  
cccccttctcctgttctcctgggaatctatgtggtcacagtagggcaacctgggcatgattctcctgattgcagtcagccc  
tctacttcacaccccatgtactatttctcagcagctgtccttctcgcgatttctgctatttctcctgtcattactccaaaatgct  
gggtgaacttcttaggaagaagaatacaatcctttactctgagtgcatggccagctcttttcttgtggtctttgtgtggct  
gagggttacctcctgactgccatggcatatgatcgtatgttgccatctgtagccactgcttataatgcgatcatgtccta  
30 tgggtctgctactgctagtgtggtgctccttcttctgggcttctctctgcttgccttgactcatacaagtgccatgatgaaactg  
ccttttgcaatccacattatcaaccattacttctgtgatgttcttccctcctcaatctcctgctccaacacacaccta  
gagcttctacttttatcattgcgggggttaacacctgggtgccaccctagctgttgctgtctcctatgcttcatcctctacag  
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ttgggtccattacctcatgtattcaagcccttcaagtaactccctggaccaggagaagggtgctcctgtgttctacacc  
35 acggtgatccccatgctgaacctttaataacagctctgaggaataaggatgtgaagaaagcattaaggaaggcttaagg  
aggaggagacagcctagcagatgg (SEQ ID NO: 57)

MOOSE06820 ctg15944 3168536..3168548, 3217166..3218091,

40 RGRNQTEVTEFLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIV  
LIKIDLCLHTPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAA  
QFYFFGSFLGTECFLLAMMAYDRYAAIWNPLLYPVLVSGRICFLLIATSFLA  
GCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPLKLSCSDTHFNIGVIMAFSS  
FIVISCVMIVLISYLCIFIAVLKMPSLBGRHKAFTSCASYLMAVITIFFGTILFMY  
45 LRPTSSYSMEQDKVVSVFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHILHS  
PN (SEQ ID NO: 60)

cgaggcagaaatcaacagaagtaacagaatttctcctttaggactttccgacaatccagatctacaaggagt  
cctcttgcattgttctgtgatctatattggcaaacatgggtgggcaatttggggatgattgtattgattaagatgatctctgtc  
ccacacccccatgtatttcttctcagtagcctccttctttagatgctccttactcttctcctgactcccaagatgctggtga  
50 acctcatgggtgagaataaggccatttcttcatggatgtgctgccagtttacttcttggctccttctggtgggactgagt

gcttcctgttgccatgatggcatatgaccgctatgcagccatttgaaccccctgctctaccagttctcgtgtctgggag  
aatttgcttttctaatagctacctcttcttagcagggttggaatgcagccatacatagggatgacttttaggtgtcc  
tttgggttctaataaggatcaaccatttctactgtgacaccccgccactgctcaaacctcttctgctgataccacttcaatg  
gcatgtgatcatggcatttctcaagtttattgtcatcagctgtgttatgattgtcctcatttctacctgtgtatcttcattgccgt  
5 cttgaagatgccttcgttagagggcaggcacaaagccttctccacctgtgccttctacctcatgggtgtcacatattctttg  
gaacaatcctcttcatgtacttgcgcctacatctagctactcaatggagcaagacaaggttctctgtctttatacagtaa  
taatccctgtgctaaatcccctcatctatagttaaaaaataaggatgtaaaaaaggccctaaagaagatcttatgaaaca  
catcttgcacagcccaat (SEQ ID NO: 59)

10 MOOSE06827 ctg13103 26933654..26934554, 26941304..26941347,  
MEIKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLAAVGNVLIPAI  
YSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISYVGCLAQM  
YFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSIS  
HLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVLKLSGSDTSSSQMVVMTETLA  
15 VIVTPFLCHFSYLRIMVTVLRIPSAAGKWKAFTSTCGSHLTAVALFYGSIIYVY  
FRPLSMYSVVRDRVATVMYTVVTPMLNPFTYSLRNKDMKREIKKKLSKRTK  
EHSP (SEQ ID NO: 62)

atggagataaagaactacagcagcagcaccctcaggcttcatctcctgggcctctctccaaccctcagctgc  
agaaacctctcttggccatcttctcatcatgtacctgctcgtcgggtgggaatgtgctcatcatccggccatctactct  
20 gacccaggtccacacccctatgtacttttctcagcaactgtcttctcatgatactgtctcacaacagtcatagtgccta  
agatgctggtgaatttctatcagagacaaggttatctcctatgtgggctgcctggccagatgtacttcttatggcatttg  
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gttatgaaccacggcattgctgctcatgtattgggttctgcagcatctccacctacattccctgttccgctgctactt  
atgtctcgttcttctgtgcctctcacatcattaagcacttttctgtgacaccagcctgtgctaaagctcctgctctga  
25 cacatctccagccagatggtggtgatgactgagacccttagctgtcatigtgaccccttctgtgtatcatctctcctacct  
gogaatcatggtcactgtgctcagaatcccctctgcagccgggaagtgggaagccttctctacctgtgggtcccacctca  
ctgcagtagccctttctatgggagtattattatgtctatttaggccctgtccatgtactcagtggttagggaccgggtagc  
cacagttatgtacacagtagtgacaccatgctgaaccctttcatctacagcctgaggaacaaagatatgaaggaggaga  
tcaagaagaactctcaaaacgaacaaaggaactcccc (SEQ ID NO: 61)

30 MOOSE06828 ctg14877 4363377..4363409, 4364445..4365350,  
MKRKNFTEVSEFIFLGFSSFGKHQITLFFVFLTVYILTLVANIIVTII  
DHHLHTPMYFFLSMLASSETVYTLVIVPRMLLSLIFHNQIPISLAGCATQMFFF  
VILATNNCFLLTAMGYDRYVAICRPLRYTVIMSKGLCAQLVCGSFGIGLTM  
35 AVLHVTAMFNLPPCGTVVDHFFCDIYPVMKLSCIDTTINEINYGVSFVIFVP  
IGLIFISYVLVISSILQIASAEGRKKTFTATCVSHLTVVIVHCGCASIAYLKPKSE  
SSIEKDLVLSVITYITPLNPPVYSLRNKEVKDALCRVLSKRHRYGNI (SEQ  
ID NO: 64)

atgaagagaaagaactcacagaagtgtcagaattcatttcttgggatttctagcttggaaagcatcagataa  
40 ccctcttctgtggtttcctaactgtctacatttaactctggttgtaacatcatcattgtgactatcatctgacttgaccatcatct  
ccacactcccatgtatttcttctaagcatgctggctagttcagagacggtgtacacactggcattgtgccacgaatgcttt  
gagcctcattttcataaccaacctatctccttggcaggctgtgtctacacaaatgtcttttcttcttggccactaataattg  
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actatgtgccagctggtgtgtgggtccttggcattggtctgactatggcagttctccatgtgacagccatgttcaattggc  
45 gtctgtggcacagtggtagaccacttcttgtgacattaccagtcataaacttcttgcattgataccactatcaatgag  
ataataaattatggtgaagttcatttctgattttgtgcccataggcctgatatttatctcctatgtcctgtcatctctccatct  
tcaaattgcctcagctgagggccggaagaagaccttggccacctgtgtctcccacctcactgtggtattgtccactgtggc  
tgtgcctccattgctacctcaagccgaagtcaagaagttcaatagaaaaagacctgttctctcagtgacgtacaccatca  
tcaactccctgtgaaccctgttgtttacagtctgagaaacaaggaggtaaaggatgccctatgcagagtacttctaagag  
50 acacaggtatggaaacatc (SEQ ID NO: 63)

- 73 -

MOOSE06832 ctg13517 2024387..2025309, 2050457..2050472,  
MAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMITLI  
CLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNISYAGCMSQL  
5 YFFLVFVIABCYMLTVMAYDRYVAICHPLLYNIIMSHHTCLLLVAVVYAIGL  
IGSTIETGLMLKLPYCEHLISHYFCDILPLMKLSCSSSTYDVEMTVFFSAGFNII  
VTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHLAAVGMFYGSTAFMYLK  
PSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGKLSPHSW  
(SEQ ID NO: 66)

10 atggctgcaggaaatcactctacagtacacagagttcattctcaagggttaacgaagagagcagacctccagc  
tcccccttttctcctctcctcgggatctacttggtcaccatcgtggggaacctgggcatgatcactctaattgtctgaactc  
tcagctgcacacccccatgtactactttctcagcaatctgtcactcatggatctctgtactcctcgtcattaccctaaatgat  
gctggtgaactttgtgtcagagaaaaacatcatctcctacgcagggtgcatgtcacagctctacttctcctgtttttgtcatt  
gctgagtggtacatgctgacagtgatggcctacgaccgctatgttgccatctgccacccttggctttacaacatcattatgtct  
15 catcacacctgcctgctgctggtggctgtggtctacgccatcggactcattggctccacaatagaactggcctcatgttaa  
aacggcctattgtgagcacctcatcagtcactacttctgtgacatcctcctctcatgaagctgctctgctagcacctatg  
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ccagcatcctcggcatcagcaccacagaggggagatccaaagcctcagcacctgcagctcccacttgcagccgtgg  
gaatgttctatgatcaactgcattatgtactttaaaccctccacaatcagttccttgaccaggagaatgtggcctctgtg  
20 ttctacaccacggtaatccccatgttgatccccctaattctacagcctgaggaacaaggaagtaaggctgcctgcagaa  
aacgctgaggggtaactgagcccgcatctctgg (SEQ ID NO: 65)

MOOSE06837 ctg15944 5082071..5082579, 5123054..5123489,  
MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLD  
25 SHLHTPMYFFLSNLSLAGIGYSSAVTPKVL TGLLIEDKAISYSACAAQMFFCA  
VFATVENYLLSSMAYDRYAAVCNPLHYTTTMTTRVCACLAIGFTGSYICGL  
FOSSIHVAFTFHL SFCHSNV VNHFFCDIPLLALSCSDIYAHEIVL FILAAFNIF  
FTLLIILNSYVFIFAILRMHSAEGQKKVFSTCAYHLTTVSIFYGTITFMYLQPS  
SGHSMDDTKISSVFYTMVIPMLNPLVYSLRNKEVQSAFKVVIGKAKSSLGL  
30 (SEQ ID NO: 68)

atggagaataatacagaggtgagtgaaattacctccttggtctaaccaatgccccagaactacaggtccct  
ctttatcatgtttaccctcatctacccatcactctgactgggaacctggggatgatcatattaatcctgctggactctcatctc  
cacactccccatgtactttttctcagtaacctgtctctgcaggcattggttactcctcagctgtcactccaaaggttttaactgg  
gttgcttatagaagacaaagccatctcctacagtgctgtgctgctcagatgttctttgtgcagctttgccactgtggaaaa  
35 tiacctctgtcctcaatggcctatgaccgctacgcagcagtggtgaacccctacattataaccaccacatgacaacacgt  
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gagattgtgctctcatattggcagcatttaatacttttactctcttgattatctgaactcttatgtttttattttattgctatcct  
gaggatgcattcagctgagggacaaaaaaggtctttccacctgtgcctatcacctcactactgtttccatctctatggga  
40 caatcacctttatgtacttacagccaagttctggtcattccatggacacagacaaaatctcatctgtgtttacaccatggtca  
tccccatgcttaaccctctagtctatagcctgaggaacaaagaagtcagagtgcatcaaggtggttattggaaaagcaa  
agtcttcattgggcta (SEQ ID NO: 67)

MOOSE06838 ctg15944 6676490..6676496, 6679052..6679971,  
45 6713800..6713814,  
MESWNSSSVTMFILLGFTDHPQLALLFVTFLLGIYLTTLAWNLAFLI  
RGDTHLHTPMYFFLSNLSFDICYSSAVAPNMLTDFWEQKTISFVGCAAQF  
FFVGMGLSECLLLTAMAYDRYAAISSPLLYPTIMTQGLCTRMVVGAYVGG  
FLSSLIQASSIFRLHFCGPNINHHFFCDLPPVLALSCSDTFLSQVVNVLVVTV  
50 GGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTALFV

YLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKIP  
SPW (SEQ ID NO: 70)

atggaatcctggaacagctcatcagtgaccatgttcatcctcctgggattcacagaccatccagaactccagg  
ccctcctcttttgaccttctgggcatctatcttaccacctggcctggaacctggccctcattttctgatcagaggtgaca  
5 cccatctgcacacacctatgtacttctcctaagcaactatcttctgacatctgctacttctgctgtggtcccaatag  
ctcactgacttcttctgggagcagaagaccatatcatttgggctgtgctgctcagtttttcttctgctggcatgggtctgtc  
tgagtgcctcctcctgactgctatggcatacaccgatatgcagccatctccagcccccttcttaccctactatcatgacc  
cagggcctctgtacacgcatggtggtggggcatatggtggtggtcctgagctccctgatccaggccagctccatattta  
ggcttacttttgcggaccaacatcatcaaccacttcttctgcacctcccaccagctcctggtctgtcttctgtacacc  
10 ttctcagtcagtggtgaatttctcgtggtggtcactgtcggaggaaacatcgttctccaactcctatctcctatggttac  
atagtgtctgcggctcctgaagatcccttcagcagagggccgatggaaagcctgcaaacacgtgtgcctcgcactgtatggt  
ggtgactctgctgttgggacagcccttctgttacttgcgacctcagctcagctacttctagggaggagacaagggtgt  
gtctgttttctattcattggtgatcccatgctgaacctctcattacagtttgaggaacaaagagatcaaggatgcctgtg  
gaagggtgttgaaaggaagaaaattccttaccctgg (SEQ ID NO: 69)

15 MOOSE06839 ctg4256 15048207..15049148,  
MDGTNGSTQTHFILLGFSDRPHLERILFVILIAAYLLTLVGNTTILVSR  
LDPHLHTPMYFFLAHLSFLDLSFTTSSIPQLLYNLNGCDKTISYMGCAIQFL  
FLGLGGVECLLLAVMAYDRCVAICKPLHYMVIMNPRLCRGLVSVTWGCGV  
20 ANSLAMSPVTLRLPRCGHHEVDHFLREMPALIRMACVSTVAIEGTVFVLKK  
GVVLSPLVFILLSYSYTVRAVLQIRSASGRQKAFGTCGSHLTVVSLFYGNIIY  
MYMQPGASSSQDQGMFLMLFYNIVTPLLNPLIYTLRNREVKGALGRLLLGK  
RELKKE (SEQ ID NO: 72)

atggatggaaccaatggcagcaccacaaaccatttcatcctactgggattctctgaccgacccatctggaga  
25 ggatcctcttttggtcatcctgatcgcgtacctcctgacctcgtaggcaacaccaccatcatcctggtgtcccggctgga  
ccccacctccacacccccatgtacttctctcgcaccaccttcttctgacctcagttcaccaccagctccatcccc  
agctgctctacaaccttaatggatgtgacaagaccatcagctacatgggctgtgccatccagctcttctgttctgggtct  
gggtggtgtgagtgctcttctggtgtcatggcctatgaccggtgtgtggtatctgcaagccccctgactacatggt  
gatcatgaacccccaggctctgccggggtgtgtcagtgacctggggtgtgggtggccaactccttgccatgtctc  
30 ctgtgacctgcgcttaccctgctgtgggaccacagaggtggaccacttctgctgagatgcccgccctgatccggat  
ggcctgcgtcagcactgtggccatcgaaggcaccgtcttctgctgaaaaaagggtgtgtgtgtgtcccccttggtgttctc  
ctgctctcttacagctacattgtgagggctgtgttacaattcggctcagcatcaggaaaggcagaaggccttcggcacctgc  
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ccagggcaggttctcctatgctcttctacaacattgtacccccctcctcaatcctctcatctacacctcagaacagagag  
35 gtgaagggggcactgggaagggtgtcttctggggaagagagagctaggaaaggag (SEQ ID NO: 71)

MOOSE06841 ctg15944 2976120..2976989, 3039328..3039399,  
MSRRNYTELTEFVLLGLTSRPELRAPCFGVFLVIYLVTVLGNLGLITLI  
KIDTRLHTPMYYFLSHLAFVDLCYSSAITPKMMVNFVVERNTIPFHACATQL  
40 GCFLTTFMITECFLASMAIDCYVAICSPLHYSTLMSRRVCIQLVAVPYIYSFL  
VALFHTVITFRLTYCGPNLINFYCDLPLALSCSDTHMKEILIFAFAGFDM  
ISSSSIVLTSYIFIAAILRIRSTQGQHKAI STCGSHMVTVTIFYGTLIFMYLQPK  
SNHSLD TDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQI  
(SEQ ID NO: 74)

45 atgtccagaagaactatactgaactgacagaattgttcttgggtctaacaagccgtccagagctgcgagc  
cccggtcttggggtgttttagttatctatctgggtcacagtgtgggcaatcttgggttgattactttaatcaagattgatactc  
gactccacacacctatgtactatttctcagccacctggccttgggttgaccttgggttactcctctgctattacaccgaagatgat  
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gagtggttcttctagcctccatggcctacgattgctatgtgccatctgtagtccctgcattattcaacactgatgtcaaga  
50 agagtctgcattcaactgggtggcagttccatataatacagcttctggttgccttctccacaccgttatcatttccgtctga

- 75 -

cttactgtggcccaacttaattaaccatttctattgtgatgacctccccttcttagctctgtcctgctcagacacacacatgaa  
ggaaattctgataattgccttctgtggcttgatgatctcttcttccattgtcctcacctcctacatttattattgccgcta  
tcctaaggatccgctctactcaggggcaacacaaagccatttccacctgtggctcccatatggtagctgctactatttctat  
ggcacactgactttatgtacctacagcccaaatcaaatcactccttgacacagacaagatggcttctgtatttacacagt  
5 ggtgatccccatgttaaacccttaattctatagctaaaggaacaaagtgaaagatgcctcaaagaaagccttgata  
aaggtgtgaaaacttacagata (SEQ ID NO: 73)

MOOSE06843 ctg13517 1713448..1713473, 1723011..1723498,  
1781840..1782270,

10 MTLRNSSSVTEFILVGLSEQPELQLPLFLFLGIYVFTVVGNLGLITLIG  
INPSLHTPMYFFLFNLFSIDLCSVFTPKMLNDFVSESIISYVGCMTQLFFFC  
FFVNSECYVLVSMA YDRYVAICNPLLYMVTMSPRVCFLILMFGSYLMAFS  
GAMAHTGCMLRLTFCDANTIDHYFCDILPLLQLSCTSTYINELVVFTVVGINI  
15 IVPTVTIFISYGFILSSILHISKEGRSKAFSTCSSHIIA VSLFFGSGAFMYLNPSS  
AGSMDKRKLSSVFYTNVPMNLPLIYSLRNKDVKFALRKALRRRHKLSDI  
(SEQ ID NO: 76)

atgactctgagaaacagctcctcagtgactgagttatccttgtgggattatcagaacagccagagctccagct  
ccctcttttcttctattcttagggatctatgtgtcactgtggtgggaacttgggtgatcaccttaattgggataaatccta  
gccttcacacccccatgtacttttcttcaactgtccttatagatctctgttattcctgtgtgtttacccccaaatgctgaa  
20 tgactttgttcagaaagtatcatctcttattgtgggatgtatgactcagctattttcttctgtttcttgaattctgagtgtatgt  
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gagctggtggtttcactgtggttgcatcaacatcattgtgccactgttaccatcttattcttattgtttcatcctctccag  
25 catctccatcatcagttccaaggaggcaggtccaagcttcagcacttcagttcccatataattgctgtttctctgttctt  
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ggttcccatgttgaacccttaattctacagcctgaggaacaaagatgttaaattgccctaagaaaagccctgagacgaag  
gcataagttatctgatatt (SEQ ID NO: 75)

30 MOOSE06844 ctg15907 32272575..32273514,

MWINNQSSLDFFILLGFSDRPWLETPLSVIFLVAYIFSLFGNISILVSH  
LDPQLDSPMYFFVSNLSFLDLCYTTSTVPQMLVNLRGPEKTISYGGCVAQLY  
IFLALGSTECLLAIMAFDRYAAICKPLHYPMNMHRRCIHMAAGTWISGFAN  
SLVQSTLTVVAPRCGQRVLDHFFCEVPALLKLACIDIRVNEMELNVLGALLL  
35 LMPLTLILGTYVFIAQAVMRICSAESRWKAFNTCASHLLVVSIFYFTAISMY  
VQPPSSYSHDRGKIMALFYGIVTPTLNPFIYTLRNKDVKAALRRSLTKEFWIK  
TR (SEQ ID NO: 78)

atgtggatcaacaatcaaagctcgtatgattttatcctattgggattttctgaccgtccctggctagagacac  
ccctctctgtaattttctggtggcctacatcttttccattttgaaatatctccattatcctagtttcccatctggatcccagc  
40 ttgacagtcctcatgtactttttgtcttaattctatcctttctggacctctgctataccaccagcactgtcccacagatgctggtc  
aacctccggggaccagaaaagaccattagctatgggggtgtgttgcccaactctatatattttggccctgggttctactg  
aatgcatacttctagccatcatggcctttgaccgttacgctgccatgcaagcccttcactaccagtcacatgaaccat  
agacgctgtatccacatggctgctggcacttgatcagtggtttgtaactccttgcctcagtcacacitcagtggtgg  
cccaagatgtggacagaggggtgtggaccatttctctgtgaagttccagccctttgaaactagcctgtattgatattctg  
45 tgaatgaaatggagctcaatgtactaggcgtttgcttctctgatgccactaccctcatcctgggcacttatgtgttcattg  
ctcaggcagtaatgagaatctgctctgctgaagtcgctggaaggctttcaataacctgtgcctcacattgtggtgtctc  
cctcttctacttcacagccatcagtatgtatgtccagcctccctctagctattctcatgaccgggggaagatcaggtctctt  
ttatggcattgtcacaccacccctcaaccattcatctacacattgagaacaaggatgtgaagctgccctgagaaggctc  
actgactaaagattttggattaagacaaga (SEQ ID NO: 77)

50



MOOSE06845 ctg15944 2844959..2844965, 2848633..2849564,

5 MGRNRNTNVPDFIL TGLSDSEEVQMALFILFLLIYLTMLGNVGMILII  
RLDLQLHTPMYFFLTHLSFIDLSYSTVITPKTLANLLTSNYISFMGCF AQMFF  
FVFLGAAECFLLSMAYDRYVAICSPLYPVIMSKRLCCALVTGPYVISFINS  
FVN VVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEIMHILAGSTLM  
VSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMTFTYLKPR  
KSYSLGRDQVASVFYTTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSSQW  
(SEQ ID NO: 80)

10 atgggtagaagaaataacacaaatgtgcctgactcatccttacgggactgtcagattctgaagaggccagat  
ggccctcttatactatttctcctgataacctaatactatgctggcaatgtggggatgattgataatccgctggacctc  
cagcttcacactcccatgtattttcttactcactgtcatttattgacctcagttactcaactgtcatcacacctaaacctta  
gcgaacttactgacttcaactatatttcttcatgggctgcttggccagatgttcttttcttctggagctgctgaatgt  
tttctctcatcaatggcctatgatcgctacgtatctgcagtcctctacgttaccagttattatgtccaaaaggctgt  
gttgcgctcttgcactgggcccctatgtgattagctttatcaactcctttgtcaatgtggttggatgagcagactgcattctg  
15 cgactcaaagtgtgtcacttttctgcgacacgtctccaatttagctctgtcctgcattgacacatacgacattgaat  
catgatacacattttagctggtccaccctgatgggtgccttaccacaaatctgcacccatgtgtccattctctaccatcc  
tgaataaattaccacttcaggaaagcagaagccttctactgtgcctctcatctcttggagtcaccaatctttatggaac  
tatgattttactattttaaaaccaagaagcttattcttgggaaggatcaagtggcttctgttttatactattgtgattccc  
atgctgaatccactcatttatagcttagaacaagaagtaaaaaatgctctcattagatcatgcagagaagacaggact  
20 ccagtcagtgg (SEQ ID NO: 79)

MOOSE06848 ctg15944 3080567..3080584, 3085575..3085701,  
3152600..3153396,

25 MLSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIR  
TNSQLQTPMYFFLGHLSFVDICYSSNVTNMLHNLSEQKTISYAGCFTQCL  
LFIALVITEFYFLASMAIDRYVAICSPHYSSRMSKNICISLVTVPYMYGFLN  
GLSQTLLTFHLSFCGSLEINH FYCADPPLIMLACSDTRVKKMAMFV VAGFTL  
SSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCMYVRPP  
SEKSVEQSKVIAVFYTFVSPMLNPIIYSLRNKDVKQAFWKILRRNQICFLW  
30 (SEQ ID NO: 82)

atgtgtccccaaaccacaccatagtgacagaattcattctcttaggactgacagacgacccagtgttagagaa  
gatcctgtttggggtgtcctggcgatctacctaatacactggcaggcaacctgtgcatgatcctgctgacaggaccaat  
tcccaactgcaaacacccatgtatttcttcttggcactctcctttgtagacatttctatttccaatgttactccaaatag  
ctgcacaatttctctcagaacagaagacatctcctacgtggtgcttcacacagtgtcttctctcatcgccctagtgt  
35 cactgagtttacttcttgcctcaatggcattggatcgtatgtagccattgcagccctttacattacagttccaggatgtcc  
aagaacatttgcattctctgtgcactgtgccttacctatgtatggcttctaatgggctctctcagacactgtgacctttact  
tatccttctgtggctcccttgaaatcaatcatttctactgcgctgacccctcttattatcatgtggcctgctctgacaccgtgtc  
aaaaagatggcaatgtttgtagtgcaggcttactctcctcaagcctctcttcatcattcttctgtcctatctttcattttgcag  
cgatcttcaggatccgttctgctgaaggcaggcacaagcctttctacgtgtgcttccacctgacaatagtcatttgttt  
40 atggaacctcttctgcatgtacgtaaggcctccatcagagaagtcagtggaacagtcgaaagtcattgctgttttctacact  
tttgaagccctatgttgaacccatcatctatagtttgaggaacaaggatgtgaacaagccttttgaaactgacagaag  
aaaccagatttgtttctctgg (SEQ ID NO: 81)

MOOSE06850 ctg18037 4716900..4717012, 4725887..4726711,  
4748336..4748345,

45 MGGNQTSITEFLLLGFPIGPRIQMLLEGLFSLFYIFILLTLMGNGIILGLI  
YLD SRLHTPMYVFLSHLAIVDMSYASSTVPKMLANLVMHKKVISFAPCILQ  
TFLYLAFATECLILVMMC YDRYVAICHPLQYTLIMNWRVCTVLA STCWIFS  
FLLALVHTLILRLPFCGPQKINHFFCQIMSVFKLACADTRLNQVVLFA GSAFI  
50 LVGPLCLVLVSYLHILVAILRIQS GEGRRKAFSTCSSHLCVVG LFFGSAIVMY

- 77 -

MAPKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSIS  
YW (SEQ ID NO: 84)

atggggggaaatcagacttccatcacagagttcctcctactgggatttccattggcccaaggattcagatgct  
cctctttgggctcttccctgttctacatcttattctttaaaccctgatgggaaatgggattatcctggggctcatctacttg  
5 actctagactgcacacacccatgtatgtcttctgtcacacctggccattgtggacatgtcctatgccctcagactgtccct  
aagatgctagcaaatcttggatgcacaaaaagtcctccttgcctcctgcatactcagactttttgtattggcgtttgct  
attacagagtgtctgatttggatgatgtgciatgatoggtatgtggcaatctgtaccccttgcataacacccctattatga  
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ctgcctttttgtggccacaaaagatcaaccactttttgtcaaatcatgtccgtattcaaatggcctgtgctgacactagg  
10 ctcaaccagggtgtcctatttgcgggttctgcgttcatcttagtggggccgctctgcctggtgtggtctcctactgcacat  
cctggtggccatcttgaggatccagcttggggaggggccgcagaagggccttctacctgtcctcccacctctgcgtgg  
tggggcttttcttggcagcgcattgtcatgtacatggccccaagtcaagccattcacaagaacggaggaagatcctttc  
cctgttttacagcctttcaaccgcatcctgaacccctcatctacagccttaggaatgcagagggtgaaaggggctctaaa  
gagagtcctttggaacagagatcaataagtattgg (SEQ ID NO: 83)

15 MOOSE06860 ctg15944 2680355..2680361, 2682467..2683101,  
2712158..2712469,

MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFVTLGNLGLITLI  
RMDSQLHTPMYFFLSNLAFIDIFYSSTVTPKALVNFQSNRRSISFVGCFFVQMY  
20 FFMFCFVFLGTABCYLLSSMAYDRYAAICSPHYTVIMPKRLLCLALITGPYVI  
GFMDSFVNVVSMRSLHFCDNIIHFFCDTSPILALSCTDNTDNTMLIFIIAGS  
TLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTMIFTYL  
KPRKSYSLGRDQVAPVFYTVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR  
KW (SEQ ID NO: 86)

25 atggctggcaacaatttactgaggttaccgtcttcatcctctctgattgcaaatcacctgaattacaagtca  
gtcttttctgtatgttcttcttattatctattcactgttttgggaaacctgggactgacacgttaacagaatggattctcagct  
tcacacccctatgtacttttctgagcaatttagcattattgacatatttactcctctactgtaacacctaaaggcattggtgaa  
ttccaatccaatcgagatccatctcctttgttggctgctttgttcaaatgtactttttatgttctgttttcttgggtactgc  
tgaatgttatcttctcctcaatggcctatgatcgcctatgcagcgcagctgcagctcctacactacacagtattatgccaaa  
30 aggcctctgcctcgcctcactggtccttattgtattggttattgagactccttgcctatgtggttccatgagcagattgc  
atttctgtgactcaaacataattcatcacttttctgtgacacttcccaatttagctctgtcctgcactgacacagacaact  
gaaatgctgatattcattatcgtgttccacctgatggtgtccctatcacaatatctgcacctatgtgtccattctctac  
catcctgaaaattaattccactcaggaaagcagaagcttctcacttgcctctcatcttgggagtcaccatcttctat  
ggaactatgattttacttactaaagccaagaaagtcttattccttgggaagagatcaagtggctcctgtgtttatactattgt  
35 gattcccatgctgaatccactcattatagcttagaagagagaagtgaaaaatgctctcattagagtcagagagaaga  
caggactccagaaaatgg (SEQ ID NO: 85)

MOOSE06861 ctg13517 1596125..1597057,

MAAENHSFVTKFILVGLTEKSELQLPLFLVFLGIYVTVTLGNLGMITL  
40 IGLSSHLHTPMYCFLLSLSFIDFCHSTVITPKMLVNFVTEKNISYPECMTQLY  
FFLVFAIAECHMLAAMAYDGYVAICSPLLYSIIISNKACFSLILVVYVIGLICA  
SAHIGCMFRVQFCKFDVINHYFCDLISILKLSCSSTYNELLILFSGINILVPSL  
TILSSYIFIASILRIRYTEGRSKAFSTCSSHISAVSVFFGSAAFMYLQPSSVSSM  
DQKGKVSSVFYTVVPMLNPLIYSLRNKDVHVALKKTTLGKRTFL (SEQ ID  
45 NO: 88)

atggcagcagaaaaccattctttgtgactaagtttattctggttgggctaacagagaagtcagagctacagctg  
cccccttctcctgttcttctgggaatctatgtatgcacagtgtggggaacctgggcatgatcacactgattgggtcagtt  
ctcacctgcacacacctatgtactgttctcagcagctgtccttcttacttctgctcattccactgtcattaccctaagat  
gctggtgaactttgtgacagagaagaacatcatctcctaccctgaatgatgactcagctctacttcttctcgttttgcatt  
50 gcagagtgtcacatgttggctgcaatggcatatgacggctacgtggccatctgtagcccttctgtacagcatcatcatat

ccaataaggcttgctttctctgatttagtggtgtatgtaataggcctgatttgcgtcagctcatataggctgtatgttagg  
gttcaattctgcaaattgatgtgatcaaccattattctgtgatcttattctatcttgaagctctcctgttctagctactacattaat  
gagttactgatttaattcttagtggaattaacatccttgccccagcctgaccatcctcagctcttacctctcatcattgccag  
catcctccgcatcgtactgagggcaggtccaaagccttcagcacttcagctcccatctcggctgtttctgtttct  
5 ttgggtctgcagcattcatgtacctgcagccatcatctgcagctccatggaccaggggaaagtgtcctctgtgtttatact  
attgtgtgcccatgctgaacccctgatctacagcctgaggaataaagatgtccacgttgccctgaagaaaacgctagg  
gaaaagaacattctta (SEQ ID NO: 87)

MOOSE06863 ctg13517 1850676..1851026, 1878547..1879134,  
10 MTLRNSSSVTEFILVGLSEQPELQLPLFLFLGIYVFTVVGNLGLITLIG  
INPSLHTPMYFFLFNL SFIDL CYSCVFTPKMLNDFVSESIISYVGCMTQLFFFC  
FFVNSECYVLVSMAYDRYVAICNPLLYMVTMSPRVCFLLMFGSYVVGFA G  
AMAHTGSMLRLTFCDSDNVIDHYLCDVLP LLQLSCTSTHVSELVVVLIVVGIN  
IMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
15 SSGSMEQGVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRNIF  
(SEQ ID NO: 90)

atgactctgagaacagctcctcagtgactgagttatccttggtggattatcagaacagccagagctccagct  
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gccttcacacccccatgtacttttctctcaactgtcctttatagatctctgttattcctgtgtgtttacccccaaatgctgaa  
20 tgactttgttcagaaagtatcatctcttatgtgggatgtatgactcagctattttctctgtttcttgaattcagtgctatgt  
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25 ttcataatcaatccactcaaggaagatcaaaagccttcagctctgtagctctcatgtcattgctctgtctctgtttttgggtca  
gcggcattcatgtatattaatattctcttgatcatggagcagggaaaagtttctctgtttctacactaatgtggtgccat  
gctcaatcctctcatctacagtttgaggaaacaggatgtcaaggtgcactgaggaaagctctgattaaaattcagagaag  
aaatatattc (SEQ ID NO: 89)

MOOSE06866 ctg15944 2354182..2355090, 2359348..2359383,  
30 MGKENCTTVAFILLGLSDVPELRVCLFLLFLLIYGVITLLANLGMIAL  
IQVSSRLHTPMYFFLSHLSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQF  
YLFCTCVVTEVFLLAVMAYDRFVAICNPLLYTVTMSWKVRVELASCCYFC  
GTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVNETLLFLVATL  
35 NESVTIMILTSYLLILTILKMGSAGEGRHKAFTSCASHLTAITVFHGTVLSIYC  
RPSSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKCVVWRKRI  
MSSK (SEQ ID NO: 92)

atgggcaaggaaaactgcaccactgtggtgagttcattctccttgactatcagatgtccctgagtgagagt  
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40 cggctccacacccccatgtacttttctcagccactgtcctctgtagattctgctactcctcaataattgtgccaaaatgtt  
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45 agacactgctgttctggtggccacttgaatgagagtgttaccatcatgatcatcctcactcctacctgctaattctacca  
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cacagtcgtgattcctatgctgaactctgtgatctacagcctgagaataaagatgtgaaagaagctctcagaaaatgtgtg  
gtgtggaggaaaggattatgtccagcaaa (SEQ ID NO: 91)

50

MOOSE06868 ctg15944 2805857..2805868, 2810804..2811415,  
2834798..2835118,

MDQGNKTEVTMFILTGFTDDFELQVFLFLLFFAIYLF TLIGNLGLVVL  
VIEDSWLHNP MYFSLSVLSFLDACYSTV VTPKMLVNFLAKNKSISFIGCATQ  
5 MLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASVVA  
GILHATHIVATFSLSFCGSNEIRHVFCDMPPLLAISCS DHTNQ LLLFYFV GSI  
EIIVTILIVLISYGFILLAILKMQSAEGRRKVFSTCGAHLTGVTIYHGTILFMYV  
RPSSSYTSDNDMIVSIFYTTVIPMLNPITYSLRNKDVKEAIKRLLV RNWFINKL  
(SEQ ID NO: 94)

10 atggaatcaagggaacaagactgaagtcaccatgtttatattgacaggcttcacagatgatttgagctgcaagtc  
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15 gtgccactcatcactgcttctacgttgctggcattttacatgctactatacatatagtggtacatttagcctgtcctctgtgg  
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20 ccatgctgaatcccatcattacagtttgcggacaaaagatgtaaaggaggcaatcaaaagattgctgtgagaattgggt  
cataaataagtta (SEQ ID NO: 93)

MOOSE06874 ctg13103 7821645..7821689, 7841845..7842762,

MEWENQTLVEFFLK GHSVHPRLLELFFVLIFIMYV VILLGNGLILISI  
25 LDPHLHTPMYFFLG NLSFLDICYTTSIPSTLV SFLSERKTISFSGCAVQMFLG  
LAMGTTECVLLGMMAFD RYVAICNPLRYPIMSKNAYVPM AVGSWFAGIV  
NSAVQTTFFVQLPFCRKNVINHFSC EILAVMKLACADISGNEFLMLVATILF  
TLMPLLLIVISYSLIIS SILKIHSSSEGRSKAFSTCSAHLTVVHIFYGTILFMYMKP  
KSKETLNSDDL DATDKIISMFGVMTPMMNPLIYSLRNKDVKEAFIKCLLY  
30 VKTLCCSD (SEQ ID NO: 96)

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35 gagtgtgtcttctggcatgatggccttgaccgctatgtggtatctgcaaccctcagatatcccatcatcatgagca  
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40 attctatgggaccatccttctcatgtatatgaagcccaagctaaagagacacttaattcagatgacttggtgctaccgaca  
aaattatatccatgttctatgggtgatgactcccatgatgaatccttaattctacagcttagaacaaggatgtgaaagag  
gcaticattaagtgtcttcttattgtgaagacatttgttgcagac (SEQ ID NO: 95)

MOOSE06875 ctg14877 3368510..3369409, 3379949..3379990,

MDTGNWSQVAFIILGFPHLQGVQIYLFLLLLLIYLM TVLGNLLIFLV  
45 VCLDSRLHTPMYHFV SILSFSSELGYTAATIPKMLANLFSEKKTISFSGCLLQIY  
FFHSLGATECYLLTAMAYDRYLAICRPLHYPTLMTPTLCAEIAIGCWLGGLA  
GPVVEISLISRLPFCGPNRIQHVFCDFFPVL SACTDTSTNVLVDFVINSCKIL  
ATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHLTVVLIFYGSILSMYVRL  
50 KKSYSLDYDQALAVVYSVLT PFLNPFYSLHNKEIKEAWKKYICRRQPATE

## M (SEQ ID NO: 98)

atggacacaggggaactggagccaggtagcagaattcatcatcttgggcttccccatctccagggtgtccag  
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cggttcacacacccatgtaccactttgtcagcattctctctctcagagctggctatacagctgccaccatccctaagat  
5 gctggcaactgttgcagtgagaaaaagaccatttcattctctgggtgtcctgcagatctatttcttactccctggagc  
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10 atcatctgcacagtgtcagaattccctcagctgccggcaagaggaaggccatctccacgtgtgctccaccctcactgt  
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gcagtgtgtactcagtgctcacacccttctcaacccctcatctacagctgcacaacaaggagatcaaggaggcttg  
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15 MOOSE06877 ctg183 49657..49676, 57650..58571,

MSGENVTKVSTFVLVGLPTAPGLQYLLFLLTYLFLVLENLAIIIV  
WSSTSLHRPMYYFLSSMSFLEIWYVSDITPKMLEGFLLQOKRISFVGCMTQL  
YFFSSLVCTECVLLASMA YDRYVAICHPLRYHVLVTPGLCLQLVGFVSVGF  
TISMIKVCFISSVTF CGSNVLNHFCDISPILKLACTDFSTAELVDFILAFIILVF  
20 PLLATILSYWHITLAVLRIPSATGCWRAFSTCASHLTVVTVFYTALLFMYVR  
PQAIDSQSSNKLISAVYTVVTPINPLIYCLRNKEFKDALKKALGLGHWLHP  
W (SEQ ID NO: 100)

atgagtggggagaatgtcaccaaggcagcaccttcatcctggtgggcttccccacggccccagggtgtgca  
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25 cacctccctccacaggcccatgtactacttctgagctccatgtcttctcggagatctgtgacgtgtcgtacatccccc  
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30 acggacttctccactgcagagctgtgtgattcatcctggccttcatcctcctggtgttccgctcctggccaccatactgtc  
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gccttgaaaaaggccttgggcttgggtcattggctccatccctgg (SEQ ID NO: 99)

35 MOOSE06878 ctg14667 1179150..1179156, 1180308..1181239,

MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTHIALSWL  
DLRLHTPMYFFLSHL SLLDLCFTTSTVPQLLINLCGVDRITTRGGCVAQLFIY  
LALGSTECVLLVMAFDYAAVCRPLHYMAIMHPHLCQTLAIASWGAGFV  
40 NSLIQTGLAMAMPLCGHRLNHFCEMPVFLKLACADTEGTEAKMFVARVIV  
VAVPAALILGSYVHIAHAVLRVKSTAGRRAFGTCGSHLLVFLFYGSAIYT  
YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDKVKGALWKVLWRGRD  
SGQW (SEQ ID NO: 102)

atgggaagttcaacaccagtttgaagatggctcatttgggtgggattctcagattggccgcaactggagccc  
45 atcctgtttgtcttattttatttctactccctaactctcttggcaacaccatcatcatcgtctctcctggctagacctcggct  
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50 ggccatgcctctctgtggccatc gactgaatcacttctctgtgagatgcctgtatttctgaagttggctgtgcggacacag

- 81 -

aaggaacagaggccaagatgtttgtggcccagtcagtgctgttctgcagcacttattctaggctcctatgtgc  
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cctttttatactataattacccccattctcaatctctcatttatacactaagaacaaggacgtgaagggggctctgtggaa  
5 agtactatggaggggcagggactcagggcagtg (SEQ ID NO: 101)

MOOSE06882 ctg4256 15474228..15474921, 15514483..15514700,  
15525055..15525087,

MDTGNKTL PQDFLLLGFPQSQT LQLSLFMLFLVMYILTVSGNVAILM  
10 LVSTSHQLHTPMYFFLSNLSFLEIWTAAVPAKALAILGRSQTISFTSCLLQ  
MYFVFSLGCTEYFLLAAMAYDRCLAICYPLHYGAIMSSLLSAQLALGSWVC  
GFVAIAVPTALISGLSFCGPRAINHFFCDIAPWIALACTNTQAVELVAFVIAV  
VVILSSCLITFVSYYIISTILRPSAIEGKRKAFSTCSSHLTVVTLYYSPVIYTYI  
RPASSYTFRDKVVAALYTLVTPTLNPVMVYSFQNRMQAGIRKLLHSKRNY  
15 HQS (SEQ ID NO: 104)

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20 agagtacttctcctggcagccatggcttatgaccgtgtcttgcctatctctatcctttacactacggagccatcatgagta  
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25 agtggtgacccttactatctcctgtaatctacacctatataccgccctgttccagctatacattgaaagagacaagggtgtg  
agctgcactctatacttctgtactcccacattaaaccgatgggtgtacagcttccagaataggagatgcaggcaggaat  
taggaagcttctgcacagcaaaagaactatcatcagagt (SEQ ID NO: 103)

MOOSE06887 ctg15944 6600325..6601250, 6608365..6608383,

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIR  
30 MDSHLHTPMYFFLSNLSFIDVCYISSTVPKMLSNLLQEQQTITFVGCIIQYFIF  
STMGLSESLMTAMAYDRYAICNPLLYSSIMSPTLCVWMVLGAYMTGLT  
ASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQVMTAILTMFFG  
IASALVIMISYGYIGISIMKITSAGRSKAFNTCASHLTA VSLFYTS GIFYLSS  
35 SSGGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRNWGSSNW  
(SEQ ID NO: 106)

atgactgggggaggaatattacagaaatcacctatttcatcctgctgggattctcagatttccaggatcataa  
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45 catcatgaagatcacttcagctaaaggcaggtccaaggcattcaacacctgtgcttctcatctaacagctgtttccctcttct  
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ctggggaagctcaaactgg (SEQ ID NO: 105)

MOOSE06888 ctg30162 162624..163103, 175517..175972,

MKKEQDSNVTEFVLLGLSSSWELQLFLFLLFFFYIAIVLGNLLIVVT  
VQAHAILLQSPMYFLGHLSFIDLCLSCVTVPKMLGDFLQQKSSISFSGCLA  
QIYFLHFLGASEMFLLTVMAYDRYVAICNPLRYLTVMNPQLCLWLVLACW  
5 CGGFIHSIMQTLTTFQLPFCNAQVIDHYFCDVHPVLKLACADTTLINMLVVA  
NSGLISLGCFLLLASYSKVVLLSLQKQSAESRRKALSTCGSHLTVVTFFFVPCI  
FIYLRPSTTFPLDKAVSVFYTTITPMLNPLIYTLRNEDVKNAMRQLWSSKISL  
KEK (SEQ ID NO: 108)

10 atgaaaaagaacaagattctaattgtgacagaattgttcttctgggcctatcatcttctgggagctgcagctatt  
tctcttctactattttgtttttacattgctattgtcctgggaacctcttgatagtggttaacagtgcaagcccatgctcacctg  
ctccaatctcctatgtatttttttaggtcatctctcttcatgacatgacctgagctgtgttactgtgccaagatgtaggg  
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15 ccttctgtaatgctcaggtatagaccatttctgtgatgtccaccagtcctaaaactgacctgtgctgatacaactctgat  
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tggtgaaccactcatctatactctgaggaatgaggatgtaaagaatgcatgaggcagctatggagtagcaagatctcct  
20 tgaaggaaaa (SEQ ID NO: 107)

MOOSE06889 ctg30162 1516718..1516750, 1570040..1570948,

MKGANLSQGMFELLGLTTDPQLQRLLFVVFLGMYTATLLGNLVMF  
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25 QMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVCASLIVGSYSA  
GFLNSLIHTGCFSLKFCGAHVVTHFFCDGPPILSLSCVDTSLEILLFIFAGFN  
LLSCTLTILISYFLILNTILKMSSAQGRFKAFTSCASHLTAICLFFGTTLFMYLR  
PRSSYSLTQDRTVAVIYTVVIPVLNPLMYSLRNKDVKKALIKLLTCMFSPTR  
W (SEQ ID NO: 110)

30 atgaaaggggcaaacctgagccaagggatggagttgagctcttgggcctcaccactgacccccagctcca  
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agtgccaccctgcacacacctgtactccctcctgaagagcctcctcttctggatttctgctactcctccaggttggcc  
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35 atcatgtctcctgaggtctgtgctcgtgattgtgggctcctacagtgacaggttctcaattctcttatccactggctgt  
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40 ctgtcatctacacagtggtgatccagtgctgaacccctcatgtactcttgagaacaaggatgtgaagaagctttaat  
aaagtactactctgtatgtttcccccacaagatgg (SEQ ID NO: 109)

MOOSE06891 ctg14877 3511302..3511312, 3527441..3528371,

MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLTSNVFIHAI  
45 RLDShLHTPMYFLSFLSFSSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQM  
FFSASWACTNCFLLAAMGFDRYVAICAPLHYASHMNP TLCAQLVTSFLTG  
YLFGLGMLTVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPSELRIFLSLVL  
LVSFFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRP  
KASYSLERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGSQW  
50 (SEQ ID NO: 112)

atggggcagaccaacgtaacctcctggaggagatttcttctcctgggcttctccagttctggggagttgcagct  
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 cttcagaggggagattgtggtgggagccagtgg (SEQ ID NO: 111)

MOOSE06899 ctg15944 2268933..2269865,  
 15 KNQTAGVTFILLGFSEFPDLQIPLFLVFLTYTTITVMGNLGMIMVIRINP  
 KLHTPMYFFLSHLSFVDFCYSTTTITPKLLENLVVEDRIISFTGCIMQFFFACIFV  
 VTETFM LAAMAYDRFVAVCNPLLYTVAMSQR LCSLLVAASYSWSLVC SLT  
 YTYFLLT LSF CRTNF INNFVCEHAAIVA VSCSDPYMSQKVILVSATFNEISSV  
 VIILTSYAFIFITVMKMPSTGGRKKAFTSCASHLTAITIFHGTLFLYCVPNSKS  
 20 SWLMVKVASVFYTVVIPMLNPLIYSLRNKDVKETVRKLVTITKLLCHKM  
 (SEQ ID NO: 114)

aaaaatcagactgctggagtcaccttcatcttctgggcttctcagaatttccagaccttcagataccctgttcc  
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 30 gatgccttccactggggggcgaagaaagcgttctccacgtgtgcctccacctgaccgccattaccattttccatggga  
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MOOSE06901 ctg15944 4763657..4764577, 4783485..4783520,  
 35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAI  
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 GCLSQLFIFTFLGATECFLLAAMAYDRYVAICMPLHYGAFVSWGTCIRLAA  
 ACWLVGFLTPILPYLLSQLTFCGPNVIDHFSCDASPLLALSCSDVTWKETVD  
 40 FLVSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTSCAHLTVVSLF  
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MOOSE06904 ctg15285 7136188..7136217, 7137011..7137334,  
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10 GATEFYLLASMSYDRYVAICKPLHYLTIMSSRVCIQLVFCSWLGGFLAILPPI  
LMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMISVMTATIVFIMIPFS  
LIVTSYIRILGAILAMASTQSRKVFSTCSSHLLVVSLLFFGTASITYIRPQAGSS  
VTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLVEGKHSHPV (SEQ  
ID NO: 118)

15

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25 cacagtcacacacctgctcaacccatctacacccctcggaaacaggacgtgaggagggcctgcgacacttg  
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MOOSE06908 ctg15944 3578921..3579826, 3636467..3636502,

MTLGNSTEVTEFYLLGFGAQHEFWCILFIVFLLIYVTSIMGNSGILLIN  
30 TDSRFQTLTYFFLQHLAFVDICYTSATPKMLQSFTEENLILFQGCVIQFLVY  
ATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRVTCIRLVAGSYIMGSINA  
SVQTGFTCSLSFCKSNSINHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFT  
GLVVIFYTYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTLASYMYLQSH  
SNNSQENMKVAFIFYGTVIPMLNPLIYSLRNKEVKEALKTLLKRRHLCSQQ  
35 (SEQ ID NO: 120)

atgacactaggaaacagcactgaagtcactgaattctatcttctgggatttggtgccagcatgagtttggtgta  
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45 acactcttctacatgtatttgagctctcatttaataatccaggaaaatgaaagtggccttattttatggcacagtatt  
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50

MOOSE06909 ctg15285 7251039..7251953, 7304530..7304565,  
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GIITATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHRSEISVMTATIVFI  
MIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLLFFGTASITYIRP  
5 QAGSSVTDDRVLSTFYTVITPMLNPIYTLRNKDVRRALRHLRLIRKKKKSSQ  
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121)

20 MOOSE06910 ctg30162 2022696..2022718, 2049308..2050235,  
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VAQLYFFHFLGSTQCFLYTLMA YDRYLAICQPLHYVLMNGRLCTVLVAG  
25 AWWAGSMHGSIQATLTFRLPYCGPNQVDYFICDIRAVLRLACADTTVNELV  
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AIHICKW (SEQ ID NO: 124)

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MOOSE06911 ctg4256 15849243..15849993, 15905554..15905744,  
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45 QHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMIAGSWF  
GGSLDGFLLTPTMSFFCNSREINHFFCEAPAVLKLACADTALYETVMYVC  
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GRFKGPQRV (SEQ ID NO: 126)

50 atgcccaattcaaccaccgtgatggaattctcctcatgaggtttctgatgtgtggacactacagattttacattct

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15 IYLDTQLHTPMYFLLSQLSLMDLMLICTTVPKMAFNYSLSGSKSISMAGCVTQ  
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VAMIASYAGVILAVIHMGSGEGRRKTFTTCSHLMVVGMYYGAALFMYTRP  
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20 (SEQ ID NO: 128)

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aagggcaagtctgagagtgaatta (SEO ID NO: 127)

40 MARENSTFNSDFLLGIFNHSPHTHTFLFFLVLAIFSVAFMGNSVMVLLI  
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(SEQ ID NO: 130)

BNSDOCID: &lt;WO\_\_\_\_\_03000735A2\_I\_&gt;

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5

MOOSE06927 ctg13910 4182589..4183512, 4253928..4253945,

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FFSFAFGGTTECFLLATMAYDRYVAICKPLLYPVIMNNSLCIRLLAFSFLGGF  
10 LHALIHEVLIFRLTFCNSNIHHFYCDIPLFMISCTDPSINFLMVFILSGSIQVFT  
IVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLLSVSLYYGPLIFMYLRPA  
SPQADDQDMIDS VFYTHIPLLNPIYSLRNKQVIDSFTKMVKRNQKHSSN  
(SEQ ID NO: 132)

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25 aat (SEQ ID NO: 131)

MOOSE06929 ctg13361 38992807..38993472, 39003872..39004156,

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30 GCALQMYLTLALGSTECLLLA VMAYDRYVAICQPLRYPELMSGQTCMQM  
AALSWGTFANSLQLSILVWHLPCGHVINIFYEILAVLKLACGDISLNALA  
LMVATAVLTLAPLLLICLSYLFILSAILRVPSAAGRCKAFSTCSAHRTVVVVF  
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LRGGLLSRKA (SEQ ID NO: 134)

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atggagccgctcaacagaacagaggtgtccgagttcttctgaaaggattttctggctacccagccctggagc  
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133)

MOOSE06931 ctg4256 14682446..14682793, 14711763..14712371,

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BNSDOCID: <WO 03000735A2 I >

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10 aaagtactaggagatgtggttctctccagagcatc (SEQ ID NO: 139)

20 atggcagagatgaacctacaccttggtagccaggttctctcttattgcattcactgaatatcctgaatgggcactc  
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acctgtttatcatttggccatcctgcagatccactctgctggaggccgggccaagacccttctccacctgcgcctcccacc  
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30 gagtgtgtctgtgctctacacgggtgtgaccccaatgctgaatccccttatctatagcctgagaacaaggaggtaaaa  
gaggccactagggaaggccctgagcaaatcaaggcctgctagaagaccc (SEQ ID NO: 141)

atgaaacaggaaatcaagatttgggacagattttctacttgttggtcttttcaatatggctggataaactctctt  
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ctccacactccaatgtactttctgctcagtcagctctccatcgttgacctcatgtacatctccaccacagtcccagaatggc  
agtcagcttctctcacagagtaagaccattagattttgggctgtgagattcaaacgtatgtgtcttggcccttgggtgaac  
45 tgaagcccttctccttggttttatgtctatgatcgtatgtagctatctgtaccctttacattatcctatgcttatgagcaagaa  
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50 gcaaccactctctttacctacacaagggccacactccttgcgttccccctcacgggataaggcgggtggcagtattttacacca

ttgtcacaccttactgaacccatttatctacagcctgagaaataaggaagtacgggggcagtgaggagactgttggga  
tattggatatgctgtagaaaatat (SEQ ID NO: 143)

MOOSE06952 ctg22fin2 127652..127674, 157267..158171, 190073..190089,  
5 MERKNRFAFVNEFILQGFSCEWTIQIFLSLFTTTYALTTGNGAIAFV  
LWCDRLHTPMYMLGNFSFLEIYWVSSTVPKMLVNFLSEKKNISFAGCFL  
QFYFFSLGTSECLLLTVMAFDQYLAICRPLLYPNIMTGHLYAKLVILCWVC  
GFLWFLPIVLISQMPFCGPNIDHVVCDPGRFALDCVSAPRIQLFCYTLSSL  
VIFGNFLFIGSYTLVLKAMLGMPSSSTGRHKAFTSCGSHLAVVSLCYSSLMV  
10 MYVSPGLGHSTGMQKIETLFYAMVTPLFNPLIYSLQNKEIKAALRKVLGKK  
QFCSKM (SEQ ID NO: 146)

atggaaaggaaaaaccgcttggctttgtaaatgaatttatactccaagggttcttctgtgagtggaacattcagat  
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gcgacttcacactcccatgtacatgttcotgggaatttctccttttagagatatggtatgtctctctacagttccaagatgt  
15 tggtaacttcttctcagagaaaaaacatctccttggctggtgttctcagttttatttcttcttcttgggtacatcaga  
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ctgtttgtctacactctaagctcattgatttttggtaacttctccttatttggatcctatactctgtcctgaaagctatgttg  
20 ggtatgccttcaagcactgggagacataaggccttctctacctgtgggtctcattggctgtggtatcactgtgctatagctc  
tcttatggtcatgtatgtgagccaggactcggacattctacaggatgcagaaaattgaaacttgttctatgctatggtga  
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cagtttgcagcaaatg (SEQ ID NO: 145)

MOOSE06953 ctg30162 417211..418141,  
25 MDKNQTEVMREFFLSGFSQTPSIEAGLFVLFVFFYMSIWVGNVLMV  
TVASDKYLNSSPMYFLLGNLSFLDLCYSTVTPKLLADFFNHEKLISYDQCI  
VQLFFLHFVGAAEMFLLTVMAYDRYVAICRPLHYTTVMSRGLCCVLVAAS  
WMGGFVHSTVQTLTVHLPFCGPNQVENTFFCDVPPVIKLACADTFVIELLM  
30 VNSGLISTISFVVLISYTTILVKIRSKEGRRKALSTCASHLMVVTLFFGPCIFI  
YARPFSTFSVDKMVSVLYNVITPMLNPLIYTLRNKEVKSAMQKLWVRNGLT  
WKK (SEQ ID NO: 148)

atggataaaaacaaacagaagtgatgagagaattttctgtcagggttctcacagacaccatctattgaagca  
gggctatttgtactatttcttctctatgtccattgggtggcaatgtcctcatcatgtgcacagtagcatctgataaatac  
35 ctgaattcatcacccatgtatttcttcttggcaacctctcatttctggacctatgtattcaacagtaacgaccctaagcttct  
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40 tgcattgaattgctcatggtatctaacagtgggtgatccaccatctccttgggtgctgatttctcctacaccatctc  
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gcttacttgaaaaag (SEQ ID NO: 147)

MOOSE06954 ctg15944 3276061..3276997,  
45 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLI  
CNDSCSLHTPMYFFTGNLSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFF  
FSAGLAYSECYLLAAVAYDRYVAISKPLLYAQAMSIKLCALLVAVSYCGGF  
50 INSSIITKKTFSFNFCRENIIDFFCDLLPLVELACGEKGGYKIMMYFLLASNV

ICPAVLILASYLFITTSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYTYALPR  
SSYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLSHKSRLSP  
(SEQ ID NO: 150)

5 atgcagaggagcaatcatacagtgactgagttatactgctgggcttcaccacagaccaggaatgcagctg  
ggcctcttcgtggtgttcctgggcgtgtactctctcactgtggtaggaaatagcaccctcatcgtgtgatctgtaatgactc  
ctgcctccacacacccatgtatttttactggaaatctgtcgtttcggatctcgtgtattctctgtctacaccccaagatcc  
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10 ctttaactctgccgtgaaaacatcattgatgacttttctgtgatttgctcccttggtggagctggcctgtggcgagaaggg  
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acactgtggtattccccatgtgaatctcatgaictacagcctaagggaataaggatgtgaaagaggctctgaaaaaacttct  
15 ctcacataaataagattatctccacca (SEQ ID NO: 149)

MOOSE06957 ctg13910 4016560..4017448, 4027068..4027121,

MAEENKILVTHFVLTGLTDHPGLQAPLFLVFLVIYLTIVGNLGLMAL  
IWKDPHLHTPIYFLGSLAFADACTSSSVTSKMLINFFLSKNHMLSMACAT  
20 QFYFFGSNATTECFLLVVMAYDRYVAICNPLLYPVVMSNSLCTQFIGISYFIG  
FLHSAIHVGLLFRITFCRSNIHYFYCEILQLFKISCTNPTVNILLIFISAFIQVF  
TFMTLIVSYSYILSAILKKKSEKGRSKAFSTCSAHLISVSLFYGTLFFMYVSS  
RSGSAADQAKMYSLFYTHIPLNPFYSLRNKEVHRCIRNLLICRFIFIS (SEQ  
ID NO: 152)

25 atggcagaagaaaataagattctggtgactcacttgtcctcacaggactcacagatcatccagggtgcagg  
cgccccgttctggtgttcttggtcatctacctcatcaccctggtgggcaacctggcctgatggctctcatctggaagga  
ccccaccttcacacccccatacttattcttggcagtttagccttgcagatgcatgcacttcacctctgtaacttctaag  
atgcttatcaattttttatcaagaatcatatgctatccatggctaagtgtgccaccagtttacttttggttccaatgaa  
ccacagaatgcttctgctggttagtgatggcctatgaccgctatgtagccatgcaatccctgctttatcagtggtgatg  
30 tccaatagcctctgtactcagtttataggtatttcatattttatggtttctgcatcagcgattcatgtgggttgttatttagatta  
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gaaaaagaagtctgagaagggtagaagcaaaagccttctacttgcagtgcccatctgctctctgctcttctgttctacggc  
accctcttctcatgtatgtgagttctaggtctggatcagctgcagatcaggccaaaatgtattcttattttacacaataataat  
35 tccttactaaatccctttattacagcctaagggaacaagagggtcatagggtgcataagaaacttactgatatgtagattcat  
atttttatttct (SEQ ID NO: 151)

MOOSE06959 ctg13464 3864087..3864422, 3883462..3884061,

MVGANHSVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLIL  
40 LTVTSDPHLHSPMYFLLANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCI  
QIFFIHVIGGVEMMVLLIAMAFDRYVAVCKPLHYLTIMHPRMCILILVASWA  
IGLIHSLVQLSFVNLFPFCGPNVLDSFYCDIPQLIKLACTNTYKLQFMVTANS  
GFISLSAFLLLSYFILATLQKHSSGGSSKAVSTLSAHITVVVLFQPLIFFYV  
WPSPPTHLNKFLAIFDAIFTPFLNPVIYTFRNREMKIAIRRVFGQFMGFRKT  
45 (SEQ ID NO: 154)

atggttggggcaaatcactccgtggtgtcagagtttgtgttcctgggactaccaattcctgggagatccgactt  
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50 agatgatggtgctgctcatagccatggcctttgacagatatgtgccgtatgtaagcccttcactacctgacatcatgcat



ccaagaatgtgcattttgattctagtggtctctgggccattggtctcattcactcattggtccaattgtctttgtagtaaacttg  
cccttctgtggccctaattgtgttgacagcttttactgtgacatacctcagctcatcaaaacttgctgcacaaatacctataaa  
ctgcagttcatggttactgctaatagtgggttcatttccttgagtgctttcttctgtcctcctctctacatcttcattctggcca  
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5 ccaactgattttttctatgtatggccctctctccaacacatctgaataaattctagccatattgatgccatttcactcctttct  
gaatccagctcatctacattcaggaacagggaatgaagattgcaataaggagagtgttcgggtcaatttatgggttttaga  
aaaact (SEQ ID NO: 153)

MOOSE06965 ctg13464 3819604..3820057, 3832510..3833006,  
10 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLT  
VTSDPRLQSPMYFLLANLSINLVFCSSSTAPKMIYDLFRKHKTSIFGGCVVQIF  
FIHAVGGTEMVLLIAMAFDRYVAICKPLHYLTIMNPQRCILFLVISWIIATSSII  
GLIHSLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEFMVTVNS  
GLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFF  
15 YTWPSPTSHLDKYLAIFDAFTTFLNPVIYTFRNKDMKVAMRRLCSRLAHFT  
KI (SEQ ID NO: 156)

atggatgaagccaatcactctgtggtctctgagtttggttctctgggactctctgactcgcgaagatccagctc  
ctcctctctctcttttctcagtggtctatgatcaagcctgatggaaatctctcattgtgtaacttgacccttgaccctcgt  
ttacagtccccatgtactcctgtctggccaaccttccatcatcaatttggtattttgtctccacagctcccaagatgattta  
20 tgacctttcaggaagcacaagaccatctcttttgggggctgtgtagtcagatctctttatccatgcagttgggggaactg  
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acaccaagaactggagttcatgtcactgtcaatagtggaactcattctgtgggctcctttgtctgtgtaatttctcat  
25 ctctattctgttactggttgaaacattctctgggtgcttagccaaggccctctctacccgtcagctcatgtcactgtggtc  
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cttcgcgcatttacaagatt (SEQ ID NO: 155)

MOOSE06970 ctg30162 1054913..1054933, 1055717..1056623,  
1081348..1081364,  
MEIRNFSDPTEFVLAGLPNLNSARVELFSVFLLVYLLNLTGNVLIVGV  
VRADTRLQTPMYFFLGNLSCLEILLTSVIPKMLSNFLSRQHTISFAACITQFY  
FYFFLGASEFLLAVMSADRYLAICHPLRYPLLMSGAVCFRVALACWVGGL  
35 VPVLGPTVAVALLPFCKQGA VVQHFFCDSGPLLRLACTNTKKLEETDFVLA  
SLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAIFL  
YVRPSQSGSVDTNWAVTVITTFVTPLLNPFYIYALRNEQVKEALKDMFRKKR  
DCSFN (SEQ ID NO: 158)

atggagataaggaacttttagtgatccaacagagttcgtcctggcagggtcccaaatctcaacagcgcaaga  
40 gtggaattattttctgtgttcttctgtctatctcctgaatctgacaggcaatgtgttgattgtgggggtggaagggtgatac  
tcgactacagaccctatgtacttcttttggttaacctgtcctgctagagatactgtcacttctgtcatattccaaagat  
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45 tgccttcttctgtaagcagggtgctgtgtgtacagacttctctgcacagtggtccactgtcgcgctggcctgtgaccaa  
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gcctcattgtgctggcagtcctgagcatccctctgcttcaggccgtcagaaggccttctctacctgtacctccacttgata  
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gacagtaataacgacatttgtgacaccactgttgaatccattcatctatgcctacgtaatgagcaagtaaggaagcttga  
50 aggacatgttttaggaagaagaggactgtagctttaat (SEQ ID NO: 157)

MOOSE06974 ctg13517 1291127..1292063,

5 MKIKNHTPVTEVPLMGIPHTKGMENVLFVFLAFYLFLLGNLLLLLA  
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FFHHFLGCTECFLYTVMAYDRFAAICHPLPYTVIMKRRVCALLTLGTWTGS  
CLHASVLTLLIFKLSYCGPNEVDNIFCDIPVVLPLACADTSLARTVSFINVG  
VVALMCFLLLITSYACIVISILKISSEGRRAAFSTCSAHLTSILLFYGPVLIYL  
RPASSPWLDVSVQVLNNIVPSLNPLIYTLRNKGVKLALRKVLIQGVHNCGR  
(SEQ ID NO: 160)

10 atgaagataaagaatcacactccagtaactgaggtccccctgatgggaatccctcatacaaaggggatggaa  
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acctccacaccccatgtatttctcctgggaaacctgtctgtttgacatattttccctcagtgagttccccaaaatgat  
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15 gcagggtgtgtccctcctgacgctaggcacctggacggggagctgtctgcatgcatctgtcctcacactcctcatctta  
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cattgtatctatactgaaaatcagttcctcagaaggtaggcgagagccttcaacctgcagtgcccatctgacgtcc  
atcctgctcttctatggaccaatagtcctcatttatctccgacctgctccagcccttggctggactctgtgttcaggtgttg  
20 aataatattgtatccctccctgaatccttgatatactttgagaaacaaaggtgtaaagctggcactgagaaaggtgctc  
attcaaggagtacataattgtggaagg (SEQ ID NO: 159)

MOOSE06975 ctg180 11555451..11556386,

25 MALGNHSTTTEFLLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLMI  
RADSLHKPMYFFLSHLSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQV  
FFVFTAGTEACLLSGMAYDRHAAICRPLLYGQIMGKQLYMHVWGSWGL  
30 GFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDISRSLIALLCSTLL  
HGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRH  
LMPNSGSPIELIFSQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTR  
R (SEQ ID NO: 162)

atggccttggggaatcacagcaccatcacccaggttctcctccttgggctgtctgccgaccccaacatccggg  
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cttgtctccataagcccatgtatttctcctgagtcacctctcttctgtgatctctgcttctcctcagtcattgtgccaaagatgt  
ggagaacctcctgtcacagaggaaaaccatttcagtagagggtgctggtcaggtcttcttctgtgttgcactgcagg  
35 gactgaagcctgccttctcagggatggcctatgaccgcatgctgcatctgccgcccactactttatggacagatcat  
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gtaaacatggcttctgtgaagccaaaatcattcaccactacagctatgagatgccatccctcctccctctgtcctgctgat  
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40 agtgacactttactatggctcaggttgcctccgcatctcatgcaaaactcaggttcccccatagagttgatcttctgtgca  
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ttgaaaaatatttgaatataccagacgt (SEQ ID NO: 161)

MOOSE06977 ctg4256 15681676..15682181, 15705271..15705688,  
15721124..15721138,

45 TSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALLILLI  
HSEPRLHTPMYFFISQLALMDLMYLCVTVPKMLVGQVTGDDTISPSGCGIQ  
MFFHLTLAGAEVFLLAAMAYDRYAAVCRPLHYPLLMNQRVCQLLVSAW  
VLGMVDGLLLTPITMSFFPCQSWEIHHFFCEVPAVTILSCSDTSLYETILMYLC  
50 CVLMLLIPVTIISSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFYGAA

15 MOOSE06978 ctg4256 14815855..14816791,  
MEMRNTTPDFILLGLFNHTRAHQVLFMMVLSIVLTSLFGNSLMILLIH  
RDTGRLHTPMYFLLSQLSLMDVMLVSTTVPKMAADYLTGNKAISRAGCGV  
QIFFLPTLGGGECFLLAAMAYDRYAAVCHPLRYPTLMSWQLCLRTMSSW  
20 LLGAADGLLQAVATLSFPYCGAHEIDHFFCEAPVLVRLACADTSVFENAMY  
ICCVLMMLVPPFSLILSSYGLILAAVLHMRSTEARKKAFATCSSHVAVVGLFY  
GAAIFTYMRPKSHRSTNHDKVVSAFYSMFTPLLNPLIYSVRNSEVKEALKR  
WLGTCVNLKHQ (SEQ ID NO: 166)

25 atggagatgagaataactacccagactttatctcctgggactctttaaccacaccagagcccaccaagtctt  
cttcatgatggttctgagatcgtttgacctccctgtttggcaattccctcatgattctcctgattcaccggggacaccggcg  
gtccacacgcccattgacttctcctgagccaaactcctcatggacgtgaigctggttccaccactgtgccaaaatg  
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30 taccctgagcttccatattgcggtgcacacgagatcgatcacttctctgcgaggccccctgtgtggtgcgtttggctgt  
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ggctgtggtgggactctttatggagctgccattttacatatgagacccaaatcccacaggtccactaaccacgacaag  
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35 cctgaaacgggtgctggggacatgtgtaaacctgaaacaccag  
(SEO ID NO: 165)

MOOSE06983                      ctg15296 2052460..2053387,  
40        MENRNNVTEFVLLGLTENPKMQKIIFVVFFVITYIITVVGNALIVVTIT  
ASPSLGSPMYLFLAYLSFIDACYSSVNTPKLITDSLYGKNTILFNGCMTQVFG  
EHFFGGAEGILLTVMAYDRYVAICKPLHYMTIMNQCVYALLMGVVWMGG  
FLHATIQLFIFQLPFCGPNVIDHFMCDLNPLLNLACTDTHMLGLFIAANSGLFI  
CLLNFVLLLVSYYVILRSLRTHSLEARHKALSTCVSHITVVILFFVPCIFVYM  
45        RPAATLPIDKAVAIFYTMITPMLNPLIYTLRNAQMKNAIRKLCSRKDISGNK  
(SEQ ID NO: 168)

45 (SEQ ID NO: 100)  
atggagaataggaataacgtgacagagttgttttactagggttacagagaatccaaagatgcagaaaatcat  
atttgtgtgtttttttgtcatctatatcatcactgtggtgggaaatgcgctcattgtggtcaccatcactgccagcccatcact  
ggggtcccccatgtaccttttctggcctatctctctttatagatgcctgctattcttctgtcaataccctaagctgatcaca  
gattcactctatgaaagaacaccatcctattcaatggatgcatgactcaagctttggagaacatttcttggagggtgcag  
50 agggtaicctacttactgtgatggcctatgaccgctatgtggccatctgcaaggcccttgactatatgactatcatgaacca

- 95 -

gtgtgtgtatgccctgctaattgggagtggtgtggatgggaggtttcttcatgcaaccatacagatcctcttcatcttccaatt  
acctttctgtggctctaattgtcatagatcactttatgtgtgatctgaacctttgctcaacctgcctgcactgacacccatatg  
ctgggactcttcatgtgtccaacagtggttcatctgtgtgttaaactttgctcctgctgtgtcctatgtggfcatcttgcg  
ctccctaaggactcacagcttgaggcaaggcacaagccctctccacctgtgtctccacatcacagttgcatcttatic  
5 tttgtccctgcatattgtgtacatgagacctgcagctactttacattgataaagcagttgctatattctacactatgataac  
tcctatgttaaacccttaattctatacttgaggaaatgccagatgaaaaatgccatcaggaaattgtgtagtagaaaggac  
atttcaggttaacaaa (SEQ ID NO: 167)

MOOSE06987 ctg14877 4245409..4246339,  
10 MKRANHTELREFVFGFSNFPEHQLTFFVFLALYTFLLAGNFILAI  
IYVDHHLHTPMYFFLSVLSTSETFYSLVPIPRMLSSLVGLSQQSISLEGCGTQIFF  
FLGFAITNCLLLAVMEYDHYVAVCNPLRYSVIMNWRVCAILASSVCATGFS  
LSLVQTVAFRLLFCTPLIEHFFCDVQPVLDLAWATPMINDILTLMSLLAITA  
PAIFLFISYVLIISTILKITSABGGKKTFATYASHLTVVIIHYGCASIAFYKPNLE  
15 NTKDQDQLISVTYTVITPLLPVVYGLRNKEVQDALQRVLGRKFFS (SEQ  
ID NO: 170)

atgaagagagccaatcacacagagtaagagagttgtttccaaggtttccaattttccagaacatcagctc  
acattttttgtgtctttctcgcctctacacattcctaactctggctggcaatttcattctggccataatctatgtgacat  
cacctccatactcctatgtacttcttttaagtgtgtatccacttcagagactttctattccctggctattatccacgatgctt  
20 ccagcctgttaggcctgagccaatccatttccctggagggtgtgggactcagatctttttttctggcttggccatcacca  
actgcctcctgctagcagtaattggaatatgactactcgtggcgtgtgcaacccacttcgatactcagtcacatgaattg  
gagggtgtgtgtatactggcatcatcagctgtgtccacagggttctcactctcactgttcagactgtggcaatttcaggt  
tgctctttgcacccactgattgagcatttcttctgtgtgtcagcctgtgttgacctggcctgggctaccccaatgatca  
atgatattctgaccttaattatgacctccttggccatcacagcccatcttctcttcatctcttattgtccttattattcca  
25 ccatttcaagatcacctcagctgaaggcgggaagaagacctttgccacctatgcatccacctcactgtgtgctattatcc  
actatggctgtgctccattgcctactcaagcccaatttgagaataccaaagatcaggatcagttatctcagtgaccta  
cactgtcataacacctttactaaacctgtgtgtatggtctgagaataaagaagtccaggatgctctgcagagagtgctg  
ggtaggaaattcttctcc (SEQ ID NO: 169)

30 MOOSE06997 ctg15944 2146092..2147018,  
MQQNNSVTEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKS  
SRTLGSMPYFFLFYLSFADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFAL  
HLFGCMEIFVLILMAVDRYVAICKPLRYPTIMSQQVCILIVLAWIGSLIHSTA  
35 QILALRLPFCGPYLLIDHYCCDLQPLLKLACMDTYMINLLLVSNSGAICSSSF  
MILIISYVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPM  
DKMVAVFYTTIGPPFLNPLIYTLRNAEVKNAMRKLWHGKIISENK (SEQ ID  
NO: 172)

atgcagcaaaataacagtgtagtgaattcatactgttaggattaacacaggatcccttgaggcagaaaatagt  
40 gtttgaatcttctaattttctatatgggaactgtgtggggaatatgctcattattgtgacctcaagtcagccggacacta  
ggaagcccatgtacttcttctattttatgtcctttgagattcttgcctttcaacttcacagcccttagattaattgtggatg  
ctctctctgaaaagaaaattataacctacaatgagtgcacacaaagctttgactacattatttggctgcatggagatct  
ttgtcctcattctcatggctgtgatcgctatgtggcactgtgaagcccttgcgttacccaacctcatgagccagcaggtct  
gcatcatcctgattgttcttgcctggatagggtctttaatacactctacagctcagattatcctggccttaagattgccttctgt  
45 ggacctatttgattgatcattatgtgtgattgcagccctgttgaaacttgcctgcatggacacttacaatgatcaacctgc  
tgttgggtgtcaacagtgagggaattgtcaagtagttcatgatttgataatttcatataattgcatcttgacactcactgagaa  
accacagtgccaaagggaagaaaaaggtctctccgttgcagctctcacataattgtagtcatcttattcttggcccatgt  
ataattcatatatacagcccccgaccactttcccatggacaagatgggtggcagttttatactattggaccaccttctc  
aatccactcatctacacactgaggaaatgcagaagtgaataatgccatgagaaagttaggcatggcaaaattatttcagaa  
50 aacaaa (SEQ ID NO: 171)

MOOSE07000 ctg15408 7625248..7626159,

EFLLLGISEDPELQPVLAGLTLSTMYLVTVLRLNLLILA VSSDSHLHTSM  
YFVLSNLRWVDIGFTSATVPMKIVDMQSHSRVISYAGCLTQMSFLVFFACIE  
5 DMLLTVMSYDQFLAICHPLHYPVIVNPHFCVFLVLVSFFLSLLDSQLHRWIV  
LQFTFFKNVEISNEVCEPSQLNLACSDSVINIIFTYLDSTMFGFLPISGILLSYY  
KIVPSILRMSLSDVKYKAFSTCGSHLAVFCLFYGAGIGVYLTSAVSPPSGNG  
VVASVMYTVVTPMLNPFYISLRNRDIQSAPWRLRSTTVESHDL (SEQ ID  
NO: 174)

10 gaattcctcctcctgggaatctcagaggatccagaactgcagcccgtcctcgtgggtgacctgtccatgt  
acctgggtcacgggtgctgaggaacctgctcatcctcgtgctcagctcgtactcccacctccacacctcatgtactcgt  
cctctccaacctgcgctgggtgacatcgggttcacctcggccacgggtcccaagatgattgtggacatgcagtcgcatag  
cagagtcacatcttatgcgggctgcctgacacagatgtcttctggctcttttgcagtgatagaagacatgctcctgactgtg  
atgtcctatgaccaattttggccatctgtcacccctgcactaccagtcacgtgaatcctcactctgtgtcttcttagttt  
15 ggtgtccttttcttagcctgttgattcccagctgcataagtgattgtgttacaattcaccttcttcaagaatgtggaatct  
ctaatttctgtgtgagccatctcaacttctcaacctgctgtctgacagcgtcatcaatatcatattcatatttagatagta  
ctatgtttggtttcttccatttcagggtaccttttcttactataaaatgtcccctccatttcaaggatgtcattgtcagatgt  
gaagtataaagccttctccacctgtggctctcactcggcagtttttcttatttacggagcaggcattggcgtgtacctgac  
ttcagctgtgtcaccacctccggcaatggtgtggtggctcagtgatgtacactgtgtgcacccccatgctgaacctttca  
20 tctacagcctgagaacaggacattcaaatgtccccgtggaggctgcgcagcacaacagtgaatctcatgatctc  
(SEQ ID NO: 173)

MOOSE07007 ctg15944 53957..54635, 59582..59592, 62271..62501,

MEPRKNVTDFVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTV  
25 TVSETLGSPMSFFLAGLTFIDIIYSSSISPRILSDLFFGNNSISFQSFMAQLFIEHL  
FGGSEVFLLLVMAYDRYVAICKPLHYLVIMRQWVCVLLLVVSWVGGFLQS  
VFQLSIYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLLVVANGGLSCTI  
AFLLLISYGVILHSLKKLRSSSEGRHKALSTCGSHITVVILFFVPCIFMYVRP  
PLTLPIDKSLTVFYTVTPMLNPLIYTLRNAEMKNAMKKLWTRKRK (SEQ ID  
30 NO: 176)

atggagccaaggaaaaatgtgactgactttgtcctcttgggcttcacacagaatccaaaggagcagaaagtac  
ttttgtatgttctgtcttctacatttgacctgggtggcaacctgtcattgtagtaccgtaactgtcagtgagacctg  
ggctaccaatgtccttcttctgtggttaacattatagatatcattatcttcatccattccccagattgattcagactt  
gttcttgggaataattccatatcctccaatttcatggccagctctttatcgagcaccttttgggtggcagaggtcttct  
35 cctgtgtgtaggcctatgaccgctatgtggccaatgtgaacccttgcattatttggtatcatgagacaatgggtgtgtgt  
tttctgtgtgtagtgcctgggtggaggatttctgcaatcagatttcaacttagcattattatgggctccattctgtggcc  
ccaatgtcattgatcatttttctgtgacatgtatcccttattgaaactggcctgcactgacacccaatgtattggcctcttagtg  
gtggccaatggaggactgtcttgactattgcgttctgtcttactcatctcttatgtgtcatcctgcactctctaaagaaac  
ttagatcaagcagtgaaaggaggcacaagccttaccacctgtggctcccatatcactgtgtgatcctcttcttgcctt  
40 tgtatttcatgtatgtgagacctccttgaccttaccattgataaatccttgactgtgtttacactgttatcacacctatgtga  
acctctaattctatactttaagaaatgcagagatgaaaaatgctatgaagaagctcggactagaaaaagaaaa (SEQ  
ID NO: 175)

MOOSE07013 ctg14326 29348918..29348945, 29359704..29360614,

MLRSTVVTQQFLLGLSEDPELQTLAGLSLSMYLVTVLRLNLLSILAV  
45 SSDSHPHTPMYFFLSNLCWADIGFTLATVPMKIVDMGSHSKVISYGGCLTQ  
MSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLS  
LLDSQLHSWIVLQFTFFKNVEISNEVCEPSQLLKLASYDSVINSIFYDNTMF  
GFLPISGILLSYYKIVPSILRISSDGKYKAFAACGCHLAVVCLFYGTGIGVYL  
50 TSAVAPPLRNGMVASVMYAVVTPMLNPFYISLRNRDIQSALWRVCNKTVES

## HDL (SEQ ID NO: 178)

atgttgcggtccacggtggtcacacagcaattcctccttctgggactctcagaggatccagaactgcagacca  
 tcttctgtgggctgtccctgtccatgtatctggtcacggtgctgaggaacctgctcagcatcctggctgtcagctctgactc  
 ccacccccacaccccatgtacttctcctcctcaacctgtgctgggctgacatcggttcaccttggccacggttcccaaa  
 5 atgattgtggacatggggtcgcataagcaagtcacatcttatgggggctgctgacacagatgtcttcttggtaacttttga  
 tgtatagtagacatgttctgactgtgatggcttatgactgctttgtagccatctgtgccctctgcactaccagtcacgtg  
 aatcctcacctctgtgtcttctcgttttggtgtccttttcttagcctgttgattccagctgcacagttggattgtgtacaat  
 tcaccttctcaagaatgtggaatctctaattttgtctgtgagccatctcaacttctcaagcttgcctcttatgacagcgtcatc  
 aatagcatattcatatatttataataactatgtttggttttctccatttcagggatccttttgtcttactataaaattgtccctcc  
 10 attctaaggatttcatcatcagatgggaagtacaagccttctcagcctgtggctgtcacctggcagttgtttgctattttatg  
 gaacaggcattggcgtgtacctgacttcagctgtggcaccacccctcaggaaatggatggcgtcagtgatgtacgct  
 gtggtcaccccatgctgaacctttcatctacagcctgagaaacaggagacattcaagtgccctgtggagggtgtgcaa  
 caaacagtcgaatctcatgatcg (SEQ ID NO: 177)

15 MOOSE07014 ctg13910 4108517..4108789, 4139748..4140401,  
 4154576..4154593,

MEEENATLLTEFVLTGLLYQPQWKIPLFLTFLVITYLITIMGNLGLIAVI  
 WKDPHLQIPMYLLLGNLAFVDAWISSTVTPKMLNNFLAKSKMMISLSECM  
 VQFFSFVISVTTECFISASMA YDRYVAICKALLYPVIMTNGLCIQLLVLSFIGG  
 20 LLHALIHEIFLRLTFCNSNIIQHFYCDIPLLKISCTDSFINFLMVFIADSIQVF  
 TIGTILISYTLVLLILKNKSVKGIQKAVSTCGAHLISVSLYYGPLVFMYVGS  
 SPQADDQDMMESLFYTVIVPLLSMIYSLRNKQVIASFTKMFKRVASKSW  
 (SEQ ID NO: 180)

atggaagaggaaaatgcaacattgctgacagagtttctcacaggactttatatcaaccacagtggaat  
 25 acccctgttctgacattcttgtaatatatctcaccatcatggggaatcttggtctgattgctgtcatctggaaagacct  
 caccttcagatcccaatgtacttactcctcgggaatttagcttttagatgcttgatcatctacagtactcacaagatg  
 ctgaataacttcttagctaagagtaagatgatgatactctctctgaatgcatggtacaatttttcttgaatcagtgaacc  
 acagaatgttttatctcggcatcaatggcatatgatgctatgtagccatttgcaaagctttactttatccagtcattatgacca  
 acggactatgcatccagctattagtcttctcatttataggtggccttctcatgctttaatccatgaaatttttattcagattaac  
 30 ctctgtaattccaacataatacaacacttttactgtgacattatcccattgttaaagatttctgactgattcttttataactttct  
 aatggttttttttgcgattcaattcaagttttaccattggaactattcttatcttatacacttgctccttataatcttaaa  
 aaataagctgtcaaaggatacaaaaagctgtctccacctgtggagctcatctcttatctgtatctttatactatgggcccct  
 tgtcttcatgtatgtgggctctgcatccccgaagcagatgaccaagatatgatggagctctattttactgtcatcgttcc  
 ttattaaattccatgatctacagcctgagaaacaagcaagtaatagcttcattcacaaaaatgttcaaaagaaatgttgcttc  
 35 caaatcttgg (SEQ ID NO: 179)

MOOSE07017 ctg15296 2084296..2085220,

MVNRNNVTEFILLGLIENPKMQKIIFVVFVYITTMIGNVLIVVTVTA  
 SPSLRSPMYFYLAYLSFIDACYSSVNAPKLITDSL YENKTILLNGCMTQVFG  
 40 HFFGGVEVILLTVMAYDRYV VICKPLHYTTIMKQHVCSLLVGVSWVGGFLH  
 ATVQILFIFQLPFCGPNVIDHFMWDLNPLLNLVCTNHTLGLFVAANS GFICL  
 LNFLLLLVSVMVILYSLRTHSLEARCKALSTCVSHITVVILFFIPCIFVYMRPP  
 ATPIDKAVAVFYTMIA PMLNPLIYTLRNAQMKNAIRKLC SRKAISSVK  
 (SEQ ID NO: 182)

45 atggtgaatagaacaatgtgacagagtttacttactggggttatagagaatccaaaatgcagaaaatcat  
 atttgtgtgtttttgtcatctacatcaccacctgataggaaatgtgctattgtggtcaccgtcactgccagcccatcatg  
 aggtcccccattgacttttacctggcctatctgtcctttatgatgctgtattcctccgtcaatgccctaaagtcatcacag  
 attcactctatgaaaacaagactatcttactcaatggatgtatgactcaagctttggagaacatttttggagggtgttgagg  
 catcctacttactgtaatggcctatgaccgtacgtggatcatctgcaagcccttgactataaccacctcatgaagcagcat  
 50 gttttagcctgctagtgggagtgcatgggtaggaggctttctcatgcaaccgtacagatcctcttcatcttccaattacct

ttctgtgtcctaattgtcatagatcactttatgtgggatctcaacccttgcctaattgtctgcactaataccacacttagg  
actcttcgttctgccaacagtgggttcatatgcctgthaaacttctctgtcctggtctcctatatgtgcatactgtactcctt  
aaggacccacagcttagaggcaaggtgcaaagccctctccacctgtgtctccacatcacagttgtcatttattctttatac  
cctgcataatttgtgtacatgagacctccagctactttaccattgataaagcagttgtgtattctacactatgatagctcctat  
5 gtaaacccttaattctacaccttgaggaatgtcagatgaaaaatgccattaggaaattgtgtagtaggaaagctatttcaa  
gtgtcaaa (SEQ ID NO: 181)

MOOSE07018 ctg14667 1532711..1533656,  
MGRWVNQSYTDGFFLLGIFSHSQTDLVLFSAVMVFTVALCGNVLL  
10 IFLIYLDAGLHTPMYFFLSQLSLMDLMLVCNIVPKMAANFLSGRKSISFVGC  
GIQIGFFVSLVGSEGLLLGLMAYDRYVA VSHPLHYPILMNQVRVCLQITGSSW  
AFGIIDGVIQMVAAAMGLPYCGSRSDHFFCEVQALLKLACADTSLFDTLLFA  
CCVFMLLLPFSIIMASYACISLGAVLRIRSAQAWKKALATCSSHLTAVTLFY  
GAAMFMYLRPRRYRAPSHDKVASIFYTVLTPMLNPLIYSLRNGEVMGALRK  
15 GLDRCRIGSQH (SEQ ID NO: 184)

atgggaagatgggtgaaccagtcctacacagatggcttctctcttggcatctttccacagccagactga  
ccttgcctctctctctcagttatgggtgtcttcacagtggccctctgtgggaatgtcctcctcatcttctcatctacctggac  
gttggaactcacaccccatgtacttctctcagccagctctccctcatggacctcatgttggtctgtaacattgtgcaaaa  
gatggcagccaacttctgtctggcaggaagtccatctcttggggctgtggcatacaaatggctttttgtctctctgtg  
20 ggatctgaggggctctgtctgggactcatggcttatgaccgtacgtggccgttagccaccacttcactatccatctc  
atgaatcagagggtctgtctccagattactgggagctcctggcccttgggataatagatggagtattcagatgggtggca  
gccatgggcttacctactgtggctcaaggagcgtggatcacttttctgtgaggtacaagctttattgaagctggcctgtgc  
agacacttcccttttgacacccctctcttggctgtgtgtctcatgtctccttcccttccatcatcatggcctctatgt  
tgcatctctctaggggctgtgtccgaatacgtctgtcagggcctggaaaaagccctggccacctgtcctccaccta  
25 acagctgtcacctcttctatggggcagccatgtcatgtacctgaggcctaggcgctaccgggcccctagccatgacaa  
gttgccctctatcttacacagcttactccatgtgaacccctcatttacagcttgaggaatggggaggtgatgggg  
gcactgaggaaggggctggaccgtgcaggattggcagccagcac (SEQ ID NO: 183)

MOOSE07021 ctg13495 316138..316149, 333772..334699,  
30 ETTNTTGFVNEFILLGFPCRWEIQILLFVVFSLIYLLTLLGNTSIICAVW  
SSQKLHTPMYILLANESFLEICCVSSDVPIMAANLISQTQSISCAGCLLRFYFF  
SMCAAECFLFSVMSFDRFPAICRPLHYPTLMTHHVCAHIFVFCWVGGCLW  
LLTPLTLISQVLFCEPNTIDHFFCDLAPLLALSCAIPGITLTCGISALIIFLTFL  
YLGTYFCVLSTVLQVPSGLGRHKAFTSCGCHLAVVSLFYGSLMVMYVSPG  
35 SGDYGHIKKFVTLFYTLSTPFFNPLIYSFRNKDMKEALKKFLNRNHTSSRW  
(SEQ ID NO: 186)

gagactactaataccactggattgtaaatgagttcatctcttgggcttccctgccgtgggagatccagatc  
ctccttttgggtcttctctcatctaccttctgacctcctaggtaacacatccatcatctgtgtgtgtggtcaagccagaa  
actccacacacctatgtacatctactggcaatttctccttctggagatctgtgtgtcagttctgacgtgccataatggc  
40 agccaatctcatctcccagacacagacatctcctgtgtgtgctgctcgggttacttcttccatgtgtgtgcag  
agtgttatttctgtcagtgatgtctttgatagggttccctgacattgttagaccttgcactatcccacctaagacccatcacg  
tttgtgtcataatttctgtatcttctgtgggtgggtggctgtctctgttattgaccccttgacactaataatcaggtcctctt  
ttgtgttccaaacactatcgaccatttttctgtatctggcacccttctgtggcactgtctgtgtcctaactggaattact  
tgacttgtgtatcatttagcgctcctcatcatcttcttacttctgtatatccttgggacttatttctgtgttctaaagcagatgct  
45 acaggtgccttcaggcttaggaaggcataaggcttctcaacttgggtgtcaccttgcgtgtagtgcctctctctatgggtc  
cttatgggtgatgtatgttagccaggtctggggactatcatgggataaagaaatttgcacttgttctatacttgtcaactc  
cattcttaactctctgatctacagttccggaacaaggatatgaaagaggcactaaagaaatttctgaggaatcgccacac  
tagctccaggtgg (SEQ ID NO: 185)

- 99 -

MOOSE07022 ctg13495 424975..424986, 442610..443537,

ETTNITGFVNEFILLGFPCRWEIQILLFVVFSLIYLLTLLGNTSIIICAVWS  
SQKLHTPMYILLANFSFLEICCVSSDVPIMAAANLISQTQSISCAGCLLRFYFFS  
MCAAECFLSVMSFDRFPAICRPLHYPTLMTHHVCAHIFVIFCWVGGCLWL  
5 L TPLTLISQVLF CGPNTIDHFFCDLAPLLALSCAPIPGITLTCGIISALIIFLTFLY  
ILGTYFCVLSTVLQVPSGLGRHKAFSTCGCHLAVVSLFYGSLMVMYVSPGS  
GDYHGIKKFATLFYTLSTPFFNPLIYSFRNKDMKEALKKFLNRNHTSSRW  
(SEQ ID NO: 188)

gagactactaatatcactggattgtgaatgagttcatcctcttgggcttcccctgccgctgggagatccagaic  
10 ctctcttttctgtctctctctcatctacctcttgaccctcctaggaacacatccatcatctgtgctgtgtggtcgaagccagaa  
actccacacacctatgtacatctactggccaatttctcctcctggagatctgctgtgtcagttctgacgtgcccataatggc  
agccaatctcatctcccagacagagcatctcctgtgctggtgctgctccggttacttctctccatgtgtgtgcag  
agtgtctatttctgtcagtgatgtctttgataggttctgctgacattgtagacatttgactatcccacctaagacccatcacg  
ttgtgtcatattttgtgatctctgtcgggtgggtggtgctctgtgtattgaccccttgacactaatatctcaggtgtctt  
15 ttgtggtccaaactatcgaccatttttctgtgatctggcacccttgctggcactgtctgtgtccaatactggaattactc  
tgactgtggtatcattagcgtctcatctcttctaccttctgtatctccttgggactatttctgtgttcaagcacagtgt  
acaggtgcttcaggcttaggaagccataaggcttctcaactgtggctgtcacctgtgtgtgtctctctctatggttct  
cttatggtgatgtatgtagccaggtctggggactatcatgggataaagaaatttgcacctgttctatcttctgaactc  
cattcttaactctctgatctacagttccggaacaaggatatgaagaggcactaaagaaatttctgaggaatgccacac  
20 tagctccaggtgg (SEQ ID NO: 187)

MOOSE07056 ctg12475 4195646..4196574, 4197205..4197226,

MESERTTMDGSPVFYLLGIPSLPETFFLPVFFIFLLFYLLILMGNALILV  
AVVAEPLSLHKPMYFFLINLSTLDILFTTTTVPKMLSLFLLGDRFLSFSSCLLQ  
25 MYLFQSFTCSEAFILVVMAYDRYVAICHPLHYPVLMNPQTNATLAASAWLT  
ALLPPIAVVRTSQMAYNSIAYTYHCFCDHLAVVQASCSDTTPQTLMGFCIA  
MVVSFLPLLLVLLSYVHILASVLRISSELEGRAKAFSTCSSHLLVVGTYYSIAI  
AYVAYRADLPLDFHIMGNVVYAILTPILNPLIYTLNRNDVKAATKIMSQDP  
GCDRS (SEQ ID NO: 190)

atggagtcagaaagaaccactatggatggctcaccgtcttctatctattgggcatcccctctctgccagagac  
30 ctctctcctcctgtgtttttatttctcctctctaccttctcatctgatgggtaatgccctgatcctgggtggcgtgtgtggc  
agagcccagcctccacaagcccatgtacttcttctgaatctctccaccttgacatcctttaccacaaccactgtcc  
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35 atgaaccacagaccaatgctaccttggcagccagtgctggttaactgccctcctcctgccatcccagcagtagtaag  
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40 catgggcaatgtggtatgtccattctcacaccaattctcaacccctcatttacacgctgagaaacagggatgtaaaggc  
agccatcaccaaatcatgtctcaagaccaggctgtgacaggagc (SEQ ID NO: 189)

MOOSE07089 ctg14145 504679..505560, 516893..516938, 566393..566433,

MPSINDTHFYPPFLLGLIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVI  
45 KTEHSLHQPMFYFLAMLMSIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQM  
FFIHMFTGMETVLLVVMAYDRFVAICNPLQYTMILTNTKISILASVVVGRNL  
VLVTPFVFLRLPFCGHNIVPHTYCEHRGLAGLACAPIKINIYGLMVISYIIV  
DVILIASSYVLILRAVFRPLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH  
RFGQNIPHYTHILLANLYVVVPPALNPVTYGRYEIHCMRNKDLKAAKKKLIH  
50 RIWKMGKN (SEQ ID NO: 192)



- 100 -

atgccttctatcaatgacacccacttctatcccccttcttctcctgctaggaataccaggactggacacttac  
 atatctggatttcttccattctgtattgtacctgattgccattgtgggaatatgaccattcttctgtatcaaaactgaac  
 atagctacaccagcccattgttacttctgcccattgttctatgattgatctgggtctgccacatccactatccccaaat  
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 5 atggagactgttctgttgggtgcatggcttatgaccgcttgttgccatctgcaacctctccagtacacatgatctcacc  
 aataaaaccatcagatcctagcttctgtggttgggaagaaatttagttctgtaacccatttgtgttctcattctgcgtctg  
 ccattctgtgggcataacatcgtacctcacacatactgtgagcacaggggtctggccgggttggcctgtgcacccattaa  
 gatcaacataatctatgggtcatgtgtattcttatattattgtggatgtgatcttaattgcctcttccatgtgcttatcctaga  
 gctgttttgccttcccttcaagatgtccgactaaaggcctcaatacctgtggttctcatgtctgtgttatgtctgtctttac  
 10 acaccagcatttttctttatgacacatcgtttggccaaacattccccactatatccatattcttttgctaaccgtatgtg  
 gttgtccacctgcccttaaccctgtcatttatggaagatatgaatacattgtatgagaataaggattaaaggcagcaaaa  
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MOOSE07094 ctg832 2478916..2478965, 2485728..2486631,  
 15 MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFI  
 IRADAALHEPMYFLAMLATIDLVLSTTLPKMLAIFWFRDQEINFFACL VQ  
 MFFLHSFSIMESAVLLAMAFDRYVAICKPLHYTTVLTGSLITKIGMAAVAW  
 AVTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDTSFNNIYGIAV  
 AMFIVVLDLLFVILSYVFIQAVLQLASQEARYKAFGTCVSHIGAILSTYTPV  
 20 VISSVMHRVARHAAPRVHILLAIFYLLFPPMVNPITYGVKTKQIRSLIKA VST  
 LRATCTT (SEQ ID NO: 194)

atgcttcccttaataatcacctcaacacatccagctgtcttttgttgtaggaattcctggttgaacacctgcat  
 gcctggatctccatccccttctgcttcttactctggccctgctaggcaactgtacccttcttctcattatccgggctgatg  
 cagccctccatgaaccatgtaccttcttctggccatgttgcaaccattgacttggcttcttcttacaacgctgcccaaaa  
 25 tgcttgcataattctggttcaggatcaggagatcaacttcttgcctgtctgtgcagatgttcttcttactccttctccatc  
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 cagacgcttccactactgccgagggccagtgattgccattgctactgtgaacacatggctgtggaaggctggcgtgtg  
 gggacactagcttcaacaatatctatggcattgtctgtggccatgttattgtggtgttgacactgcttcttctatcctgtctat  
 30 gtcttctaccttccaggcagttctccagcttgcctctcaggaggcccgtacaaggcatttgggacatgtgtgtctcacatag  
 gtgccatcctgtccacctacactccagtagtcatcttctcagtcacccgtgtagcccgccatgtgtcccctcgtgtcca  
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 agtttgattaaggcagtttcaacgtgcgagcaacatgtactaca (SEQ ID NO: 193)

MOOSE07095 ctg14145 821868..821911, 862956..863828, 891947..891977,  
 35 MAVRNGTFLLLFVLP GIPGLEAYHIWLSIPLCLIYTTAVLGNLSILIVVIV  
 MERNLHVPMYFFLSMLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQG  
 FFVHMMFVGESAILLAMAFDRFVAICAPLRYTTVLTWPVVGRIALAVITRSF  
 CIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITVNIWYGFSPVIVMVI  
 40 LDVILIAVSYSILRAVFRLP SQDARHKALSTCGSHLCVILMFYVPSFFTLLTH  
 HFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREELKRKFSSFI LKF  
 R (SEQ ID NO: 196)

atggcagtagcaaacgggacttttcttctcttttgccttcttggcatccctgggttggaggcttatcacattg  
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 45 ccttcatgtgccatgtatttcttctcctcaatgtggtggccatgagacatcctgctgtctaccaccactgtgccaaaggccct  
 agccatcttttggcttcaagcacataacattgctttgatgcctgtgtcaccacaggcttcttctcatatgatgtttgtgggg  
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 ctgcccttctgcctaaccaacattgttctcactcctactgtgagcatattggagtggtcgtttagcctgtgtgacatcact  
 50 gtaacatttggatggcttctcagtgccattgtcatggtcatcttggatgttatcctcatcgtgtgttcttactactgacatcct

-101-

cgagcagtggttcgttgcctcccaggatgctggcacaaggccctcagcaacttggtgctcccacctctgtgtcatcctta  
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tatgtggcagtgccaccaatgctgaacccattgtctatggtggaagactaagcagatacgtgaggaattaaagagaaa  
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5

MOOSE07096 ctg14145 135777..136689, 195682..195731,

MSDSNLSDNHLPDTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMYLFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGG  
CLAQMFVHSIYALESSILLAMAFDRYVAICNPLRYTTILNHA VIGRIGFVGL  
10 FRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGARLACANTVNIVYGLTV  
ALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGILVFYIPAFF  
SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRRTLRLIP  
CPFIFSDH (SEQ ID NO: 198)

atgcagattccaacctcagtgataacctctccagacaccttcttctaacagggaatcccagggtggaggct  
15 gccactcttggtgcatcccttctgtgccatgtatcttagcactggttgaaatgctgccctcatctggtcattgcc  
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ccaagatgctggcatttctgtggctccatgctggtgagatttcttgggtggatgctggccagatgtttgtgtccattctat  
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20 ggcgactcccactgtgtgtcaccgtgtcatgacacacatactgtgagcatatgggcatcgccgactggcctgtgcc  
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25 aggagcttagagaggttgattccctgtccattatttctctgatcac (SEQ ID NO: 197)

MOOSE07097 ctg832 2502047..2502070, 2543257..2544155,  
2560940..2560964,

MPKGNSCFNPTSFLLMGIPGPEASHFWIAFPFCSMYALAVLGNMVL  
30 LVVHSEPVLHQPMYFLCMLSTIDLVLCTSTVPKLLALFWAKDAEINFGAC  
AAQMFFIHGFSAVESGILLAMAFDRYLAICWPLHYGSLLSPESVGKLGAAA  
VLRGLGLMTPLTCLLARLSYCSRVAHSYCEHMAVVKLACGGTQPNNIYGI  
TAATLVVGTDSICIAVSYALILRAVLGLSSKEARAKTFGTGCSHLGVILLFYT  
PGLFSFYTQRFQHVPRHIHILLADLYLVVPPMLNPITYGMKTKQIWDGALR  
35 LLKKKKKFSSKL (SEQ ID NO: 200)

atgcccaggcaactcatgttttaacccaaccttcttctgctcatgggaattccaggcccgaggcatccca  
cttttggttgctttcccttctgtccatgtatgccctggcagtgctgggaaacatggtggtgctagtggtacattcaga  
gcctgtattgcaccagcccatgtacctgttctctgcatgtatccaccattgacctggctctgacctccactgtgcca  
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40 cagctgtagaatctggtatactgctagcaatggccttgaccgctacttagccattgctggcctctgcaatgggtcattg  
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aggaacacagccaaacaacatctatggcatcactgctgccacactggtggtgggactgactccatctgtattgctgtctc  
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45 ctgggtgtcatacttctcttacacaccaggacttcttctctacacacagcggttggccagcagctgccccggcaca  
tccacatccttctagctgaccttacctgtgtgccacccatgtcaaccccatcatctatggcatgaagaccaaacagat  
ctgggatggggccctccggcttctgaagaagaaaaatttctcctcaaagctg (SEQ ID NO: 199)

MOOSE07098 ctg832 3016603..3017389, 3027231..3027272,  
50 3037428..3037502, 3041988..3042031,

5 MNTTLFHPYSFLLLGPGLSMHLWVGFPFFAVFLTAVLGNITLFIQ  
TDSSLHHPMFYFLAILSSIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIH  
LCTGMESA VLVAMAYDCYVAICDPLCYTLVLTNKVVSVMALAI FLRPLVFV  
IPFVLFILRLPFCGHQIIPHTYGEHMGHARLSCASIRVNIIYGLCAISILVFDIIAI  
VISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFEN  
WSSTQFMKMITLSNLYVVVPPMLNPVIYGVRTKQIYVCMNKVIRKECIKLY  
(SEQ ID NO: 202)

10 atgaataccactctatttcatccttactctttccttctctggaattcctgggctggaaagtatgcactcttgggttg  
gttttcccttcttctgtgttcttgacagctgtccttgggaatatcaccatccttttctgtatcagactgacagtagtctccatc  
15 atcccatgttctacttctctggccattctgtcatctattgacccgggctgtctacatccaccatccctaaatgcttggcacctt  
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20 tatggcttatgtgccatctctatcctggctcttgacatcatagcaattgtcatttctctatgtacagatccttctgtctgtatttctact  
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tctcaticatgacctaggttgagaactggctcatctactcaatttatgaaaatgaccctgtccaatctctatgttgggt  
gccaccaatgtcaatcctgtcatatattggagtcagaaccaagcagatctatgtctgcatgaataagggtgatcaggaagg  
aatgcataatcaagcttatt (SEQ ID NO: 201)

MOOSE07099 ctg14145 230662..231537, 238866..238872, 242726..242787,  
MNNSDTRIAGCFLTGPGLQLHIWLSIPFCIMYIAALEBNGILICVILS  
QAILHEPFIYFLSMLASADVLLSTTTMPKALANLWLGYSHISFDGCLTQMFF  
IHFLFIHSAVLLAMAFDRYVAICSPPLRYVTILTSKVIGKIVTATLSRSFIMFPSI  
FLLHLHYCQINIAHTFCEHMGIAHLSCSDISINVWYGLAAALLSTGLDIMLI  
TVSYIHILQAVFRLLSQDARSKALSTCGSHICVILLFYVPALFSVFAYRFGGRS  
IPCYVHILLASLYVVPMLNPVIYGLRGKDQKNALIRSMFDDQKHLKT  
(SEO ID NO: 204)

30 atgaacaactctgacactgcatagcagggtgcttctcactggcatccctgggctggagcaactacatactg  
gctgtccatccccttctgcatcatgtacatcgctgccctggaaggcaatggcatcctaatttgtgtatcctctcccaggcaa  
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35 ggtcatitgggaagatcgtcactgccaccctgagccgcagcttcattatgtttccatccatttctccttgagcacctgc  
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ctctacgttgcattcctctatgtcaatccggttattatggactgagaggaaaggacaaaaaaatgcattaattaggtcc  
40 atgtttgatgatcagaagcatctgaaaaca (SEQ ID NO: 203)

MOOSE07101                    ctg14145 312446..312469, 327599..327638, 336013..336057,  
366812..367600, 394801..394850,  
                 MALEAQTSVSEFILMGFPGIHTFLFFVFFLLLLLFVSTIVGNITILVVVA  
45    TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMF  
      FIIHAFCMMESTVLLAMAFDRYVAICHPLRYATILTDTHAHIGVAAVVRGSL  
      MLPCPFLIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLV  
      IGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFF  
      THRFGHHVPVHHILLANVYLLLPPALNPVVYGVKTKQIQGVWKELSWKAL  
50    HLTPS (SEQ ID NO: 206)

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10 atctcttataccagccctcttctcctttttacacaccgcttggccatcacgttccagtcocatattcacattctttggccaat  
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atcctggaaagcactacatttaactccttc (SEQ ID NO: 205)

MOOSE07102 ctg14145 712888..712906, 715624..715758, 718047..718075,  
15 731046..731784, 779456..779472,  
MDKENWLSQPSFLLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII  
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MFFIHAFSSMESGVLVAMALDRYVAICHPLHHSTILHPGVIGRIGMVVLVRG  
LLLLIPFPILLGTLIFCQATIIGHAYCEHMAVVKLACSETTVNRAYGLTMALL  
20 VIGLDVLAIGVSYAHILQAVLKVPGEARLKAFTSCGSHICVILVFYLTQFI  
YISQKRIPDPVILLNHLHLLPALNPVYGVRTKEIKQGIQNLRLHLSKHW  
(SEQ ID NO: 208)

atggacaaagaaaactggctatcccagccttctttctcctggtagggattccagggttagaggaaagccagca  
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25 atccttgcaccaatctatgtacctcttctgtccatgtagctgccatcgacctgggttctggcctcctccactgcacccaaag  
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catcctgcaccaccttattccccagctctgaaccccatgtttatggtgtgagaaccaaggagatcaagcagggaatcca  
gaacctgctgaggaggttacacataagtaagcattgg (SEQ ID NO: 207)

35 MOOSE07103 ctg14145 410316..410336, 421168..421555, 422457..422479,  
440449..440970,

MNRKQTEVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIW  
QNPSLQQPMYIFLGILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAI  
40 HFFVGMESGILLCMAFDYVAICHPLRPSIVTSHACALLAVGTATFLRGVL  
LIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCGNVKVNAIYGLMVALLI  
GGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAFFSFFS  
HRFGEHIIPPSCHIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKS  
Y (SEQ ID NO: 210)

45 atgaatagaaaacagactgaggtctctgagttcatcctgctgggattcccgggcattcacagctggcaacact  
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50 tgcctgcgcatgttagctgttgggactgccacctcctgagagggtattactcattatcccttacttctcaccagcgc

- 104 -

ctgccctactgcagaggcaatatacttccccatacctactgtgaccacatgtctgtagccaaatgtcctgtggaatgtcaa  
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ctccgggcagtggtcagcctctcctcagcagatgtcggcagaaggcctttaatacctgcactgccacattgtgccatt  
gtttctctatactccagctttcttctccttcttttccaccgctttggggaacacataatcccccttcttgccacatcattgta  
5 gccaatattatctgtcctaccaccactatgaacctattgtctatgggggtgaaaaccaaacagatacagactgtgtcat  
aaggatccttcagggttctaaggatacacaatctac (SEQ ID NO: 209)

MOOSE07106 ctg14145 631211..631261, 677856..677876, 682019..682906,  
MALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTIL  
10 FIWMDPSLHQSMYFLSMLAAIDL VVASSTAPKALAVLLVRAQEIGYTVCL  
IQMFFTHAFSSMESGVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLV  
RGLLLLPFLILLRKLIFCQATIIGHAYCEHMAVVKLACSETTVNRAYGLTVA  
LLVVGLDVLAIQVSYAHILQAVLKVPNEARLKAFSTCGSHVCVILVFYIPG  
MFSFLTHRFGHHVPHHVHVLAILYRLVPPALNPLVYRRVRNKDIHA AFKH  
15 LFNKAHLAPPL (SEQ ID NO: 212)  
atggcacttagcaattccagctggaggctaccaccgcttcttttctggttaggaattccgggttagaggaaagccagc  
actggatgcactgcccctgggcacaccttacctccttgccttagtgggcaatgttaccattccttcatctggatggacc  
catccttgaccaatctatgtacctcttctgtccatgctagctgccatcgacctggttggtgctcctccactgcacccaaa  
gcccctgcagtgctcctggttctgtgccaaagagattggtacactgtctgctgatccagatgttcttaccatgcattctcc  
20 tccatggagtcaggggtactgtggccatggctctggatgctatgtagccattgtcacccttgcaccattccacaatcct  
gcatccagggtcatagggcacatcggaatggtggtgctggtgctggggaattactactcctcatcccttctcattctgttg  
cgaaaacttatcttctgccaagccaccatcataggccatgcctattgtgaacatatggctgttgaaactgctgctcaga  
aaccacagtcaatcgagcttatgggtgactgtggccttctgtggttgggctggatgctcctggccattggtgttctcatg  
cccacattctccaggcagtgctgaaggtaaccaggaaatgaggcccgactaaggcctttagcacatgtggctctcatgtti  
25 gtgtcatcctggtcttctatatccgggaatgttctccttctcactcaccgcttgggtcatcatgtacccatcacgctcatgt  
cttctggccatactgtatgccttgtgccacctgcactcaatccttctgtctataggagggtgagaaataaggatattcatgct  
gccttcaagcatctgttaacaaagcacatcttgaccgccctta (SEQ ID NO: 211)

MOOSE07107 ctg832 2378205..2378239, 2387723..2388376,  
2430076..2430315, 2439245..2439266,  
30 MDRKNQYLPSSFVLTGIPGLES LHVWLSIPFGSMYLVAVVGNVTILA  
VVKIERSLHQPMYFFLCMLAAIDLVLSTSTIPKLLGIFWFGDSSISFSACFTQM  
FFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITIRAI  
AITPLSWMVSHLPFCGSNVVHSYCEHIALARLACADPVPSLYSLIGSSLM  
35 VGSDFVAFIAASYILILKAVFGLSSKTAQLKALSTCGSHVGVMA LYLPGMA  
SIYAAWLGQDVVPLHTQVLLADLYVIPATLNPIIYGMRTKQLRERIWTCLT  
RFAFHSHW (SEQ ID NO: 214)

atggataggagaatcaatatctaccagctccttctggtcactggcatcccagggtggagtcctacacgt  
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40 cgcagcctgcaccagcccattgtacttttctgtcatgttggctgccattgacctgggtctgtacttccactataccaaa  
cttctgggaatcttctggttcggagacagctcaatcagctttagtcttcttactcagatgttttctccacttggccacag  
ctgtggagacggggctgctgctgacctggcttttgaccgctatgtagccatctgcaagcctctacactacaagagaattc  
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45 acccgtgcccagcagctctacagctgattggttctctctatggtgggctctgatgtggccttcttctgctcctctatat  
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ttatgcttctgactatctacgtggatggcatccatctatgcggcctggttggggcaggatgtagtgccttgcacacca  
agtcctgtagctgacctgtacgtgatcatccagccaccttaaatccatcatctatggcatgaggacaaacaactgcg  
ggagagaatatggacttgccctaccaggttgcgttcttctcattg (SEQ ID NO: 213)

50

-105-

MOOSE07109 ctg14145 14326..14351, 39672..40567, 75320..75345,

MALENCEHYPIFYLTSPGLEGIKHWIFIPFFMYMVAISGNCFILIIKT  
NPRLHTPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCI  
HSFSFMESSVLLMMSFDRFVAICHPLRYSVITGQQVVRAGLIVIFRGPVATP  
5 IVLLLKAFPYCGSVVLSHSFCLHQEVIQLACTDTTFNNLYGLMVVVFVTVML  
DLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVFFVPMMLGLSL  
VHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIIKLLGRKQIPK  
ES (SEQ ID NO: 216)

atggccttggaattgtgaacattaccocatattctatctcaccagcttctggttggaaggcatcaaacat  
10 ggatttcatccctttttttatgtacatggttgccatctcaggcaattgttctctgatcattattaagaccaaccctcgtct  
gcacacacccatgtactatctactatccttgctggccctcactgacctggggctgtgtgtgtccacgttgccaccactatg  
gggatcttctggttaactcccagatgtacttctggagcgtgtcaaatccagatgttctgtcatccactcttttcttcatgga  
gtcctcagtgctcctcatgatgtccttgaccgcttgttgccatctgccaccctctgaggtattcgggtcattatcactggcca  
gcaagtggcagagcaggcctaattgtcatctccggggacctgtggccactatccctattgtcctcctcctgaaggctttc  
15 cctactgtggatctgtggtcctcctccactcattttgcctgcaccagggaagtatacagctggcctgcacagataccacctt  
caataatctgtatggactgatggtgtagtttctactgtgatgtggacctgggtgtcctcgcactgtcctatggactcatcct  
gcacacagtagcaggcctggcctcccaaggaggagcagcgccgtgccttcagacatgcaccgtcatctctgtgctgtg  
ctagtattcttggccatgatggggctgtccctggtgcacogtttgggaagcatgccccacctgctattcatcttctatg  
gccaatgtctaccttttggcctcccatgcttaaccaatcatatacagcattaagaccaaggagatccaccgtgccattat  
20 caaactcctaggcagaaagcaataccaaaggaatct (SEQ ID NO: 215)

MOOSE07112 ctg832 2800705..2800746, 2848788..2849679,  
2852911..2852924,

MDRKYSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIK  
25 TERSLHEPMYLFLSMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFF  
IHCFSFLESSVLLSMAFDRFVAICHPLHYVSILTNTVIGRIGLVSLGRSVALIFP  
LPFMLKRFPYCGSPVLSHSYCLHQEVMKLACADMKANSIYGMFVIVSTVGI  
DSLLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSVIHRF  
GKQAPHLVQVVMGFMVLLFPPVMNPVYSVKTKQIRDRLWRLSCSHSGHR  
30 GW (SEQ ID NO: 218)

atggataggaagtacagcagcgttctgtctaccttctgtgctgagtggtacccctgggctggagcgcattgcaca  
tctggatctccatccactgtgcttcatgtatctggttccatccgggcaactgcacaattcttttatcattaaaacagagcg  
ctcacttcatgaacctatgtatcttctgtccatgctggtctgattgacctgggtctctcctttgcactctcctacagtc  
tgggcatcttttgggttgagcagcagaaattagccatgatgcttgccttgcagctcttttcttactgcttctcctcctc  
35 gagtctctgtgctactgtctatggcctttgaccgcttgggtctatctgccacccttgactatgtttcattctcaccaca  
cagtcattggcaggattggcctggtctctctgggtcgtagtgtagcactcattttccattacctttatgctcaaaagattccc  
ctattgtggctcccagttctctcacattcttattgtctccaccaagaagtgatgaaattggcctgtgccgacatgaaggcca  
acagcatctacggcatgtttgcatcgtctctacagtgggtatagactcactgctcctctcttcttctgtctgatcctgag  
caccgtgctgtccatgcctccagggtgagagattcaaggcccttaacacctgtgttccacatctgtgctgtgctgctc  
40 ttctacactcccatgattggcctctctgtcatccatgcttggaaagcaggcaccacacctgggtccaggtggtcatgggtt  
catgtatcttctcttctcctgtgatgaatccattgtctacagtgtgaagaccaaacagatccgggacgactatggaggc  
ttagctgttctcattctggtcaccgggggttg (SEQ ID NO: 217)

MOOSE07115 ctg832 2583967..2584016, 2596315..2597225,

MTTHNSTGSSHSFLILLSIPGLEDQHTWMSLPFFISYLVAFLGNSLIIFI  
45 ITECSLHEPMYLFLCMLAVADLILSTTVPKALAIWFYAGAISLGGCVTQIF  
FIHATFIBESGILLAMALDRYVAICDPLHYTTVLSRAKITKIGLAVVLRSCVI  
MPDVFLVKRLPFCHSNLLPHTYCEHMAVAKFACADIHVNVWYGLSVLLYT  
VVLDALLILVSYSFILYTGFHLPSPQGARQKALGTCGSPLRVISMFYLPGIFTI  
50 TQRFHHVPLHITHILLANVCVLAPPMLNPIIYGINTRQIQELQSLQRTVWRF

**KILKI (SEQ ID NO: 220)**

atgacaaccacaaactccactggtagcagccactcactcttcattctgctgagcattcctggcttagaagacca  
gcacacatggatgtctctcccctctttatttcctaccttgttgcttccttggaacagcctcatcttcatcatcactga  
atgcagcctccacgaacccatgtacctttcctctgcatgctggctggtgacctatcctgtctactaccactgtgcca  
5 aggccttagccatatttgggtctatgctggagcaatatcccttgggtgctgtgttacccaaatcttcttaccatgctacctc  
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ctcagtcgtgcaaaatcacaaagattggcttggctgtggtcctgagaagcttctgtgtgatcatgccagatgtgttctgt  
aaagcggctgccttctgccatagcaatctgtgccacatacctactgtgagcacatggctgttgccaagttgctgtgtg  
atattcatgtcaatgttgggtatggctgtgtctctctatactgtagtctagatgcttgcctatcttagtgcctatagcttc  
10 atccgtatatacaggttccacctcccccccccaaggagctcggcaaaaggctctgggcacatgtggtccccctcag  
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gctggctaattgtctgctgttggctcctccatgctgaaccccatcattatgggatcaacaccaggcagattcaagagta  
caatcactacagagaacagtttggaggttctcaaaatactgaagata (SEQ ID NO: 219)

15 MOOSE07119 ctg832 2933027..2933930, 2961725..2961774,  
MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTI  
LSVTWIESSLHQPMYYFISILAVNDLGMSLSTLPTMLAVLWDAPEIQASACY  
AQLFFIHTFTFLESSVLLAMAFDRFVAICHPLHYPTILNSVIGKIGLACLLRS  
LGVVLPPTLLLRHYHYCHGNALSHAFCLHQDVLRSLCTDARTNSIYGLCVVI  
20 ATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLIFVPVIGVS  
MVHRFGKHLSPIVHILMADIYLLPPVLNPIVYSVRTKQIPAAVRKHRRATQ  
MSKNL (SEQ ID NO: 222)

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cattcttggctctccatcctctctgtcttgcatttggtagcattatgggtaattgaccatcctgtctgtcattggatagaat  
25 cctctctccatcagcccatgtattacttattccatctagcagtgaaatgacctggggatgtccctgtctacacttcccacat  
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cactatcactactgccatggcaatgccctctcagcccttctgttgcaccaggatgttctaagattatcctgtacagatgcc  
30 aggaccaacagtattatgggcttgtgtatgcatggcacactagggtgtggattcaatcttatacttcttcttattgtctgatt  
cttaatactgtgctgatatgtcatctcgtgaagagcagctaaaggcactcaacacatgtgtatcccatatctgtgtggtgct  
tatcttcttgtgccagttattgggtgtcaatggtccatcgttgggaagcatctgtctccatagtcacacatcctcatggca  
gacatctaccttcttctccccagtccttaaccctattgtctatagtgtcagaacaaagcagattcctgcagctgtgaggaa  
acataggagagccacacagatgagcaagaatcta (SEQ ID NO: 221)

35 MOOSE07120 ctg832 2607212..2608123, 2617445..2617486,  
MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIF  
IILTKRSLHEPMYLFLCMLAGADIVLSTCTIPQALAFWFRAGDISLDRCTIQL  
FFIHSTFISESGILLVMAFDHYIAICYPLRYTTILTNALIKKICVTVSLRSYGTIF  
40 PIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYGFSILMSTVVLDVV  
LIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGRH  
IPPCIHIPLANVCILAPMLNPIYGIKTKQIQEQLRRAMKQAIGRLIV (SEQ ID  
NO: 224)

atgcctactgtaaaccacagtggcactagccacacagtcttccattgctgggcatccctggcctacaggacc  
45 agcacatgtggattctatccattcttatttctatgtcaccgcccttcttgggaacagcctgtcatcttcatatccctaca  
aagcgcagcctccatgaacccatgtaccttctctctgcatgctggctggagcagacatgtcctctccacgtgcaccattc  
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cttcatctctgagtcaggatcttgtgtgtatggccttggaccactatattgccatagctacccactgaggtacaccacca  
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50 aagattgacttctgcccagaataatatttccacacacctttgtgaacacattggcctagccaaatgcatgtaattgacatt

-107-

cgaataaacatttggtatgggtttccattctaattgacgacgggtggttagatggtgtactaattttatttctatatgctgattct  
ccatgctgtctccacatgccttctccagatgcttgccacaaagctctcaacacatttggtcccatgctgcatcatcatcct  
cttttatgggtctggcatcttcacaatccttaccagaggttgacgccacattccacctgtatccacatcccgttggttaa  
tgctgcatctggtccacatgctgaatccattattatgggatcaaaaccaagcaaatccaggaacagtgctgtagg  
5 gcaatgaaacaagccattggaagactgatagtc (SEQ ID NO: 223)

MOOSE07122 ctg832 2874415..2874462, 2880242..2880647,  
2888479..2888518, 2894733..2894766, 2907503..2907904,

MEISIFYLVGIPGLEHANIWISIPICLMYTVAILGNCTILFFIKTEPSLHEP  
10 MYYFLSMLALSDLGLSLSSLPMLRIFLNFAPGISPDACIAQEFFIHGFSAMES  
SVLLIMSFDRIAICNPLRYTSILTSARKCIFCILAFWYFGFLVITYQSLYTRNL  
RYCKKNQLSHSYCLHQDVMKLACSDNRIDVTYGGFALCLMVDFILIAVSY  
TLILKTVLGIASKKEQLKALNTCVSHICAVIFYLPINLAVVHRFARHVSPLIN  
VLMANVLLLVPPLTNPIVYCVKTKQIRDGLNVKLTRKIRCRGD (SEQ ID  
15 NO: 226)

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ttttctctccatgttggtctctctgacctgggactatccctctcctctcctaccatgtaaggattttctgttaaatgctcc  
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20 cctttgatcgcttattgcatctgcaacccctgagatacacttccatcctcaccagtgccagaaaatgtattttctgtattttg  
gccttttggtactttggaattcctgttatctacattcagctctctataaccagaaacttgagatattgcaagaaaaaccaattatc  
ccattcctactgtctccaccaggaatgcatgaagttggcctgttctgacaacagaattgatgtatctatgctttttggagca  
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25 tccaccgcttggccggcatgtctctcccctattaatgttctcatggcaaatgttctcctactgtacccactgacgaacc  
caattgtttattgtgtaaaaactaaacagattagagatggactaaatgttaaatfaacaagaaaaataagatgctggtgagat  
(SEQ ID NO: 225)

MOOSE07127 ctg18433 325800..326273,

MEPENGTRILGFLLLGLSEPELQPMFGLFLSMYLTTFVGNLLILAI  
30 CSGSHLHTPMYFFLSNLSFVDICVTSTTVPKTLNIRTQSKVITYAGCITQMY  
FFVLFIVLDSLLLTVMAYDQFVAICHPLHYTVIVNPRLCGLLVLASWIMSAL  
NSLI (SEQ ID NO: 228)

atggaaaccagagaatggtacgaggatttaggatttcttcttctgggacttccagaggaaccagaattgcagcc  
35 cgttatgtttggactcttctcctcatgtatctgacaactgtgtttggaaacctgctcatcatcctggccatctgctctggttccc  
acctccacacccccatgtaacttctcctcttaacctgtcctttgtagacatctgtgttacctccaccacagtcctcaagacac  
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ggacagcttactcttgaccgtatggcctatgaccagttgtggccatctgtcaccacctgcactacacgggtcatcgtgaac  
cctcggctctgtggactgctggttctggcgtcctggatcatgagtgccctgaattccttgata (SEQ ID NO:  
40 227)

MOOSE07139 ctg19175 1685218..1685247, 1691111..1691175,  
1691739..1691822, 1697143..1697152, 1702096..1702136, 1716968..1716987,  
1719128..1719141, 1727477..1727523, 1733801..1733869, 1734090..1734156,  
45 1745995..1746013, 1746077..1746099, 1747870..1747892, 1750716..1750733,  
1753277..1753598, 1779680..1779700,

SPFIFSGLLFQLGLLPLFFFFFFFFFFLWRLALNYLIMGICWFLHNFNSN  
VGIRLDCVTLMPRLFLSLVGPTCHISFLEGCARQWFYFFIFIMGQLDSFLLLLY  
FNFLISSHLFILMVFICNCMSIACMSLQKLLTISPLLLSFCLENIIRHFLCESVP  
50 LLLFLSCSVTRLEELMLSLTASGCVIMICFALTIVLSYIRILATVVQIRSAASRR



tctccatttatatttcagggtccttatttcaacttggggtgctccacatTTTTTTTTTTTTTTTTTTTgagatggagtc  
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5 cctgatccaaggctgctctttagtctagtagggcccactgtcacattccttttggagggttgtgctaggcagtggtttat  
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ggcagctccacctacatgcgaccaccaccgctactccccgctggaagggcgcttggtgctgtcttctactccatcct  
cataccaccctgaatccgctcatctacagcctgaggaaccaggacatgaagagagccctgtggaagctctatctccagt  
ctcactctcactcaggctgg (SEQ ID NO: 229)

Table III

## OLFACTORY GPCRs

20 #####

# Parkinson's Disease

**Locus3      Marker:D1S2842   Lod:1.26   CM RANGE of one LOD drop: 51**

25	MOOSE06931	Olfactory	DISTANCE: 5.020 Mb
	MOOSE06924	Olfactory	DISTANCE: 5.127 Mb
	MOOSE06978	Olfactory	DISTANCE: 5.153 Mb
	MOOSE06916	Olfactory	DISTANCE: 5.207 Mb
	MOOSE06949	Olfactory	DISTANCE: 5.347 Mb
30	MOOSE06839	Olfactory	DISTANCE: 5.386 Mb
	MOOSE06809	Olfactory	DISTANCE: 5.694 Mb
	MOOSE06882	Olfactory	DISTANCE: 5.812 Mb
	MOOSE06977	Olfactory	DISTANCE: 6.019 Mb
	MOOSE06935	Olfactory	DISTANCE: 6.117 Mb
35	MOOSE06911	Olfactory	DISTANCE: 6.187 Mb

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## Hypertension

40      **Locus 4**      **Marker:D11S4102**      **Lod:1.5**      **CM RANGE of one LOD drop: 17**

<b>MOOSE06983</b>	<b>Olfactory</b>	<b>DISTANCE: 11.68 Mb</b>
<b>MOOSE07017</b>	<b>Olfactory</b>	<b>DISTANCE: 11.71 Mb</b>

45 #####

## Anxiety

**Locus1 Marker:D9S1690 Lod:4.38 CM RANGE of one LOD drop: 14**

MOOSE06874      Olfactory      DISTANCE: 3.324 Mb

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5      **RA (Rheumatoid Arthritis)**

Locus1      Marker:D3S3551      Lod:3.5 CM\_RANGE of one LOD drop: 10

MOOSE07000      Olfactory      DISTANCE: -3.42 Mb

10

Locus2      Marker:D6S265      Lod:3 CM\_RANGE of one LOD drop: 6

MOOSE06803      Olfactory      DISTANCE: -2.09 Mb

MOOSE06792      Olfactory      DISTANCE: -1.00 Mb

15

MOOSE06844      Olfactory      DISTANCE: -0.75 Mb

MOOSE06791      Olfactory      DISTANCE: -0.63 Mb

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20      **COPD (Chronic Obstructive Pulmonary Disease)**

Locus1      Marker:D1S2790      Lod:3.2 CM\_RANGE of one LOD drop: 12

MOOSE06987      Olfactory      DISTANCE: -14.6 Mb

MOOSE06828      Olfactory      DISTANCE: -14.5 Mb

25

Locus4      Marker:D19S884      Lod:2.9 CM\_RANGE of one LOD drop: 20

MOOSE06786      Olfactory      DISTANCE: 8.377 Mb

MOOSE07127      Olfactory      DISTANCE: 8.483 Mb

30

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35      **OP (Osteoporosis)**

Locus2      Marker:D11S4102      Lod:2.95 CM\_RANGE of one LOD drop: 11

35

MOOSE06964      Olfactory      DISTANCE: 11.43 Mb

MOOSE06983      Olfactory      DISTANCE: 11.68 Mb

MOOSE07017      Olfactory      DISTANCE: 11.71 Mb

40

#####

45      **NIDDM (Non-insulin dep. Diabetes)**

Locus2      Marker:D5S625      Lod:3.4 CM\_RANGE of one LOD drop: 15

45

MOOSE06878      Olfactory      DISTANCE: 8.980 Mb

MOOSE07018      Olfactory      DISTANCE: 9.333 Mb

#####

**Obesity**

5 Locus4 Marker:D14S283 Lod:3.2 CM\_RANGE of one LOD drop: 12  
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 MOOSE06970 Olfactory DISTANCE: -1.57 Mb  
 MOOSE06889 Olfactory DISTANCE: -1.11 Mb  
 MOOSE06910 Olfactory DISTANCE: -0.61 Mb  
 10 Locus5 Marker:SHGC-1089 Lod:4.6 CM\_RANGE of one LOD drop: 20  
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 15

#####

**Bipolar (Genome wide scan only)**

20 Locus1 Marker:D1S434 Lod:3.3 CM\_RANGE of one LOD drop: 25  
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25 **AMD (Age-related Macular Degeneration)**

Locus2 Marker:D3S3631 Lod:2.91 CM\_RANGE of one LOD drop: 20  
 MOOSE07000 Olfactory DISTANCE: 14.51 Mb  
 30

#####

**Asthma**

35 Locus1 Marker:D3S3698 Lod:3.8 CM\_RANGE of one LOD drop: 15  
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 40 MOOSE06957 Olfactory DISTANCE: -6.63 Mb  
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 45 Locus3 Marker:D3S1292 Lod:3.8 CM\_RANGE of one LOD drop: 10  
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Locus4 Marker:D11S1887 Lod:4 CM\_RANGE of one LOD drop: 9

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5 #####  
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10 MOOSE06850 Olfactory DISTANCE: 2.355 Mb

#####  
**Schizophrenia**

15 Locus3 Marker:D5S2050 Lod:1.52 CM\_RANGE of one LOD drop: 50

MOOSE06878 Olfactory DISTANCE: 12.85 Mb

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20 #####  
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Locus1 Marker:D3S3653 Lod:2.6 CM\_RANGE of one LOD drop: 12

25 MOOSE07000 Olfactory DISTANCE: 1.291 Mb

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**Longevity**

30 Locus1 Marker:D9S1826 Lod:2.30 CM\_RANGE of one LOD drop: 15

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45 MOOSE06838 Olfactory DISTANCE: -12.5 Mb

MOOSE07056 Olfactory DISTANCE: 7.774 Mb

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**Psoriasis**

**Locus1      Marker:GDB:182383   Lod:10.61   CM\_RANGE of one LOD  
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	<b>MOOSE06844</b>	<b>Olfactory</b>	<b>DISTANCE: -2.27 Mb</b>
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10			

## CLAIMS

What is claimed is:

- 5 1. An isolated nucleic acid molecule comprising an olfactory G protein-coupled receptor (GPCR) gene, wherein the GPCR gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 10 2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 15 3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 20 4. An isolated nucleic molecule that hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 25 5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, and hybridizes to the first nucleic acid under high stringency  
30 conditions.
6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
  - (a) the nucleic acid sequences as shown in Tables I and II;

- (b) the complement of one of the nucleic acid sequences are shown in Tables I and II; or
- (c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;

5 wherein the nucleic acid molecule is operably linked to a regulatory sequence.

7. A recombinant host cell comprising the vector of Claim 6.

10 8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.

9. An isolated polypeptide encoded by the nucleotide sequence of the group of  
15 nucleic acid sequences as shown in Tables I and II, or the complements thereof.

10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino  
acid sequence selected from the group consisting of the group of amino acid  
20 sequences as shown in Tables I and II.

11. An isolated polypeptide comprising an amino acid sequence, wherein the  
amino acid sequence is greater than about 95% identical to an amino acid  
sequence selected from the group consisting of the group of amino acid  
25 sequences as shown in Tables I and II.

12. A fusion protein comprising an isolated polypeptide of Claim 2.

13. A fusion protein comprising an isolated polypeptide of Claim 11.

30

14. An antibody, or an antigen-binding fragment thereof, which selectively binds  
to a polypeptide of Claim 2, or to a fragment or variant of said amino acid  
sequence.

15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.
- 5 16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.
- 10 17. A method of identifying an agent which alters the activity of a GPCR, the method comprising:
- (a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;
  - (b) assessing the level of activity of the polypeptide or derivative or  
15 fragment thereof; and
  - (c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;
- 20 wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a GPCR.
- 25 18. An agent that alters the activity of a GPCR, identifiable according to the method of Claim 17.
19. The agent of Claim 18, where the agent is selected from the group consisting of: a GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.
- 30 20. A method of altering activity of a polypeptide encoded by a GPCR gene, comprising contacting the polypeptide with an agent of Claim 19.
21. A method of identifying an agent which alters interaction of the polypeptide



of Claim 9 with a GPCR gene binding agent, comprising:

- a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;
- b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and
- c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent that alters interaction of a GPCR gene polypeptide with a GPCR gene binding agent, identifiable according to the method of Claim 21.

23. An agent that alters interaction of a GPCR gene polypeptide with a GPCR gene binding agent, selected from the group consisting of: a second GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of a GPCR gene polypeptide with a GPCR gene binding agent, comprising contacting the GPCR gene polypeptide and/or the GPCR gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:

- a) contacting a solution containing a nucleic acid comprising the promoter region of the GPCR gene operably linked to a reporter gene with an agent to be tested;
- b) assessing the level of expression of the reporter gene; and
- c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the

agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.

- 5     26.     An agent that alters expression of the GPCR gene, identifiable according to the method of Claim 25.
27.     A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:
- 10     a)     contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
- b)     assessing expression of the nucleic acid, derivative or fragment; and
- c)     comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,
- 15     wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.
- 20     28.     The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.
- 25     29.     An agent that alters expression of a GPCR gene, identifiable according to the method of Claim 27.
30.     An agent that alters expression of a GPCR gene, selected from the group consisting of: antisense nucleic acid to a GPCR gene; a GPCR gene polypeptide; a GPCR gene receptor; a GPCR gene binding agent; a
- 30     peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.
31.     A method of altering expression of a GPCR gene, comprising contacting a

cell containing a GPCR gene with an agent of Claim 30.

32. A method of identifying a polypeptide which interacts with a GPCR gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a GPCR gene polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a GPCR polypeptide.
33. A GPCR gene therapeutic agent selected from the group consisting of: a GPCR gene or fragment or derivative thereof; a polypeptide encoded by a GPCR gene; a G-protein; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters GPCR gene expression; an agent that alters activity of a polypeptide encoded by a GPCR gene; an agent that alters posttranscriptional processing of a polypeptide encoded by a GPCR gene; an agent that alters interaction of a GPCR gene with a GPCR gene binding agent; an agent that alters transcription of splicing variants encoded by a GPCR gene; and a ribozyme.
34. A pharmaceutical composition comprising a GPCR gene therapeutic agent of Claim 33.
35. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is an isolated nucleic acid molecule comprising a GPCR gene or fragment or derivative thereof.
36. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is a polypeptide encoded by the GPCR gene.
37. A method of treating a disease or condition associated with a GPCR in an individual, comprising administering a GPCR gene therapeutic agent to the

individual, in a therapeutically effective amount.

38. The method of Claim 37, wherein the GPCR gene therapeutic agent is a GPCR gene agonist.
- 5
39. The method of Claim 38 wherein the GPCR gene therapeutic agent is a GPCR gene antagonist.
40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous GPCR gene and a nucleic acid encoding a GPCR gene polypeptide.
- 10
41. A method for assaying a sample for the presence of a GPCR gene nucleic acid, comprising:
- 15
- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid under conditions appropriate for hybridization; and
- b) assessing whether hybridization has occurred between a GPCR gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid;
- 20
- wherein if hybridization has occurred, a GPCR gene is present in the nucleic acid.
- 25
42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said GPCR gene nucleic acid.
- 30
43. The method of Claim 41, comprising amplification of at least part of said GPCR gene nucleic acid.
44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a

contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid.

45. A reagent for assaying a sample for the presence of a GPCR gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising in separate containers:

- a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid; and
- b) reagents for detection of said label.

48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and which is capable of acting as a primer for said GPCR gene nucleic acid when maintained under conditions for primer extension.

50. The use of a nucleic acid which is 100 or fewer nucleotides in length and

which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid, for assaying a sample for the presence of a GPCR gene nucleic acid.

5

51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

10

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

15

- c) capable of selectively hybridizing to said GPCR gene nucleic acid; for assaying a sample for the presence of a GPCR gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

20

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

25

- c) capable of selectively hybridizing to said GPCR gene nucleic acid; for diagnosing a susceptibility to a disease or condition associated with a GPCR.

1/261

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Sigurdsson, Gunnar Thor

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2/261

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3/261

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4/261

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5/261

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 20 25 30  
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val  
 35 40 45  
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His  
 65 70 75 80  
 Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys  
 100 105 110  
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg  
 115 120 125  
 Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met  
 130 135 140  
 Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser  
 145 150 155 160  
 Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His  
 165 170 175  
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr  
 180 185 190  
 Lys Pro Ile Glu Ala Glu Leu Phe Phe Ser Val Leu Ile Leu Leu  
 195 200 205  
 Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala  
 210 215 220  
 Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile  
 245 250 255  
 Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys  
 260 265 270  
 Met Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys  
 290 295 300  
 Leu Met Arg Phe His His Lys Ser Thr Lys Ile  
 305 310 315

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 <213> Homo sapiens

<220>  
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 <222> (1)...(945)

6/261

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 1 5 10 15

ctc tct gag gat cca gaa cta cag ccg ttc ata ttt ggg ctg ttc ctg 96  
 Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu  
 20 25 30

tcc atg tac ctg gtg acg gtg ctg gga aac ctg ctc atc atc ctg gcc 144  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45

atc agc tct gac tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc 192  
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60

aac ctg tcc tgg gtt gac atc tgt ttc agc act tgc atc gtc ccc aag 240  
 Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys  
 65 70 75 80

atg ctg gtg aac atc cag acc gag aac aaa gcc atc tcc tac atg gac 288  
 Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp  
 85 90 95

tgc ctc aca cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg 336  
 Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr  
 100 105 110

cta ctc ctg acc gtg atg gcc tat gac cgg ttt gtg gct gtc tgc cac 384  
 Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His  
 115 120 125

cct ctg cac tat atg atc atc atg aac ccc cac ctc tgt ggc ctc ctg 432  
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu  
 130 135 140

gtt ttt gtc acc tgg ctc att ggt gtc atg aca tcc ctc ctc cat att 480  
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile  
 145 150 155 160

tct ctg atg atg cat cta atc ttc tgt aaa gat ttt gaa att cca cat 528  
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His  
 165 170 175

ttt ttc tgc gaa ctg acg tac atc ctc cag ctg gcc tgc tct gat acc 576  
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr  
 180 185 190

ttc ctg aac agc acg ttg ata tac ttt atg acg ggt gtg ctg ggc gtt 624  
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val  
 195 200 205

ttt ccc ctc ctt ggg atc att ttc tct tat tca cga att gct tca tcc 672  
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser  
 210 215 220

ata agg aag ata atg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc 720  
 Ile Arg Lys Ile Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser  
 225 230 235 240

acc	tgt	gga	tct	cac	ctc	tgt	gtg	gtc	tcc	ttg	ttc	tat	gga	aca	gga	768	
Thr	Cys	Gly	Ser	His	Leu	Cys	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Gly		
245																250	255
ctt	ggg	gtc	tat	ctc	agt	tct	gct	gtg	acc	cat	tct	tcc	cag	agc	agc	816	
Leu	Gly	Val	Tyr	Leu	Ser	Ser	Ala	Val	Thr	His	Ser	Ser	Gln	Ser	Ser		
260																265	270
tcc	atg	gcc	tca	gtg	atg	tac	gcc	atg	gtc	acc	ccc	atg	ctg	aac	ccc	864	
Ser	Met	Ala	Ser	Val	Met	Tyr	Ala	Met	Val	Thr	Pro	Met	Leu	Asn	Pro		
275																280	285
ttc	atc	tac	agc	ctg	agg	aac	aag	gat	gtg	aag	ggg	gcc	ctg	ggg	aga	912	
Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly	Ala	Leu	Gly	Arg		
290																295	300
ctc	ctt	agc	agg	gca	gcc	tct	tgt	ctc	tta	cgg						945	
Leu	Leu	Ser	Arg	Ala	Ala	Ser	Cys	Leu	Leu	Arg							
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Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Phe	Ile	Phe	Gly	Leu	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
		50			55						60					
Asn	Leu	Ser	Trp	Val	Asp	Ile	Cys	Phe	Ser	Thr	Cys	Ile	Val	Pro	Lys	
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Met	Leu	Val	Asn	Ile	Gln	Thr	Glu	Asn	Lys	Ala	Ile	Ser	Tyr	Met	Asp	
			85						90					95		
Cys	Leu	Thr	Gln	Val	Tyr	Phe	Ser	Met	Phe	Phe	Pro	Ile	Leu	Asp	Thr	
			100					105					110			
Leu	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	His	
			115				120					125				
Pro	Leu	His	Tyr	Met	Ile	Ile	Met	Asn	Pro	His	Leu	Cys	Gly	Leu	Leu	
			130			135					140					
Val	Phe	Val	Thr	Trp	Leu	Ile	Gly	Val	Met	Thr	Ser	Leu	Leu	His	Ile	
145					150					155				160		
Ser	Leu	Met	Met	His	Leu	Ile	Phe	Cys	Lys	Asp	Phe	Glu	Ile	Pro	His	
				165					170					175		
Phe	Phe	Cys	Glu	Leu	Thr	Tyr	Ile	Leu	Gln	Leu	Ala	Cys	Ser	Asp	Thr	
			180					185					190			
Phe	Leu	Asn	Ser	Thr	Leu	Ile	Tyr	Phe	Met	Thr	Gly	Val	Leu	Gly	Val	
			195				200					205				
Phe	Pro	Leu	Leu	Gly	Ile	Ile	Phe	Ser	Tyr	Ser	Arg	Ile	Ala	Ser	Ser	
			210			215					220					
Ile	Arg	Lys	Ile	Met	Ser	Ser	Thr	Glu	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	
225					230					235				240		
Thr	Cys	Gly	Ser	His	Leu	Cys	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Gly	
				245					250					255		
Leu	Gly	Val	Tyr	Leu	Ser	Ser	Ala	Val	Thr	His	Ser	Ser	Gln	Ser	Ser	
			260					265					270			

8/261

Ser Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro  
           275                  280          285  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg  
           290                  295          300  
 Leu Leu Ser Arg Ala Ala Ser Cys Leu Leu Arg  
 305                  310          315

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   1                  5                  10                  15  
 gtc tca gat gat ccg gag ctc cag att ccc ctc ttc ctg gtc ttc ctg 96  
 Val Ser Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu  
                   20                  25                  30  
 gtg ctc tat ttg ctg acc gtg gca ggg aac ctg ggc atc atc acc ctc 144  
 Val Leu Tyr Leu Leu Thr Val Ala Gly Asn Leu Gly Ile Ile Thr Leu  
           35                  40                  45  
 acc agt gtt gac cct caa ctt caa acc ccc atc ctt caa att ccc atg 192  
 Thr Ser Val Asp Pro Gln Leu Gln Thr Pro Ile Leu Gln Ile Pro Met  
   50                  55                  60  
 tat tat ttt ctt agc aac tta tct ttc tta gac atc agc tgt tct aca 240  
 Tyr Tyr Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr  
   65                  70                  75                  80  
 gca atc act cct aaa atg ctg gca aac ttc ttg gca tcc agg aaa agc 288  
 Ala Ile Thr Pro Lys Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser  
           85                  90                  95  
 atc tct cct tat ggg tgt gca cta caa atg ttt ttc ttc gct tct ttt 336  
 Ile Ser Pro Tyr Gly Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe  
           100                  105                  110  
 gct gat gct gag tgc ctt atc ctg gca gca atg gct tat gac cgc tat 384  
 Ala Asp Ala Glu Cys Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr  
   115                  120                  125  
 gca gcc atc tgc aac cca ctg ctc tat act aca ctg atg tct agg aga 432  
 Ala Ala Ile Cys Asn Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg  
   130                  135                  140  
 gtc tgt gtc tgc ttc att gtg ttg gca tat ttc agt gga agt aca aca 480  
 Val Cys Val Cys Phe Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr  
   145                  150                  155                  160  
 tca ctg gtc cat gtg tgc ctc aca ttc agg ctg tca ttt tgt ggc tcc 528  
 Ser Leu Val His Val Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser  
           165                  170                  175

9/261

aat atc gtc aat cat ttt ttc tgt gat atc cca cct ctt ctg gct tta 576  
 Asn Ile Val Asn His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu  
 180 185 190

tca tgt aca gac act cag atc aac cag ctt ctg ctc ttt gct ttg tgc 624  
 Ser Cys Thr Asp Thr Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys  
 195 200 205

agc ttc atc cag acc agc act ttt gtg gta ata ttt att tct tac ttc 672  
 Ser Phe Ile Gln Thr Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe  
 210 215 220

tgc atc ctc atc act gtg ttg agc atc aag tcc tca ggt ggc aga agc 720  
 Cys Ile Leu Ile Thr Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser  
 225 230 235 240

aaa aca ttc tcc act tgt gct tcc cac ctc ata gca gtc acc tta ttc 768  
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe  
 245 250 255

tat gga gcg ctc ctg ttt atg tac tta cag ccc acc act agc tat tcc 816  
 Tyr Gly Ala Leu Leu Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser  
 260 265 270

cta gac act gat aag gtg gtg gca gtg ttt tat act gtt gta ttt ccc 864  
 Leu Asp Thr Asp Lys Val Val Ala Val Phe Tyr Thr Val Val Phe Pro  
 275 280 285

atg ttt aat cca ata att tat agt ttc aga aac aag gat gtg aaa aat 912  
 Met Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn  
 290 295 300

gct ctc aaa aag cta tta gaa aga att gga tat tca aat gaa tgg 957  
 Ala Leu Lys Lys Leu Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp  
 305 310 315

&lt;210&gt; 8

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Ala Ser Gly Asn Leu Thr Trp Val Thr Glu Phe Ile Leu Val Gly  
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Val Ser Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu  
 20 25 30

Val Leu Tyr Leu Leu Thr Val Ala Gly Asn Leu Gly Ile Ile Thr Leu  
 35 40 45

Thr Ser Val Asp Pro Gln Leu Gln Thr Pro Ile Leu Gln Ile Pro Met  
 50 55 60

Tyr Tyr Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr  
 65 70 75 80

Ala Ile Thr Pro Lys Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser  
 85 90 95

Ile Ser Pro Tyr Gly Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe  
 100 105 110

Ala Asp Ala Glu Cys Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr  
 115 120 125

Ala Ala Ile Cys Asn Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg  
 130 135 140

Val	Cys	Val	Cys	Phe	Ile	Val	Leu	Ala	Tyr	Phe	Ser	Gly	Ser	Thr	Thr
145					150					155					160
Ser	Leu	Val	His	Val	Cys	Leu	Thr	Phe	Arg	Leu	Ser	Phe	Cys	Gly	Ser
				165					170						175
Asn	Ile	Val	Asn	His	Phe	Phe	Cys	Asp	Ile	Pro	Pro	Leu	Leu	Ala	Leu
				180					185						190
Ser	Cys	Thr	Asp	Thr	Gln	Ile	Asn	Gln	Leu	Leu	Leu	Phe	Ala	Leu	Cys
				195				200					205		
Ser	Phe	Ile	Gln	Thr	Ser	Thr	Phe	Val	Val	Ile	Phe	Ile	Ser	Tyr	Phe
				210			215					220			
Cys	Ile	Leu	Ile	Thr	Val	Leu	Ser	Ile	Lys	Ser	Ser	Gly	Gly	Arg	Ser
225					230						235				240
Lys	Thr	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Ile	Ala	Val	Thr	Leu	Phe
				245					250						255
Tyr	Gly	Ala	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Thr	Thr	Ser	Tyr	Ser
				260					265					270	
Leu	Asp	Thr	Asp	Lys	Val	Val	Ala	Val	Phe	Tyr	Thr	Val	Val	Phe	Pro
				275				280					285		
Met	Phe	Asn	Pro	Ile	Ile	Tyr	Ser	Phe	Arg	Asn	Lys	Asp	Val	Lys	Asn
				290			295				300				
Ala	Leu	Lys	Lys	Leu	Leu	Glu	Arg	Ile	Gly	Tyr	Ser	Asn	Glu	Trp	
305					310					315					

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1				5			10					15						
ttc	tca	gat	cga	cct	tgg	ctg	gag	ttt	cca	ctc	ctt	gtg	gtc	ttc	ttg	96		
Phe	Ser	Asp	Arg	Pro	Trp	Leu	Glu	Phe	Pro	Leu	Leu	Val	Val	Phe	Leu			
				20		25					30							
att	tct	tac	act	gtg	acc	atc	ttt	ggc	aat	ctg	acc	att	att	cta	gtg	144		
Ile	Ser	Tyr	Thr	Val	Thr	Ile	Phe	Gly	Asn	Leu	Thr	Ile	Ile	Leu	Val			
35				40					45									
tca	cgc	ctg	gac	acc	aaa	ctt	cat	acc	ccc	atg	tat	ttt	ttt	ctt	acc	192		
Ser	Arg	Leu	Asp	Thr	Lys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr			
50				55					60									
aat	cta	tca	ctc	ctg	gat	ctt	tgt	tac	acc	aca	tgt	aca	gtc	cca	caa	240		
Asn	Leu	Ser	Leu	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Cys	Thr	Val	Pro	Gln			
65				70					75							80		
atg	cta	gta	aat	tta	tgc	agc	atc	agg	aaa	gta	atc	agt	tat	cgt	ggc	288		
Met	Leu	Val	Asn	Leu	Cys	Ser	Ile	Arg	Lys	Val	Ile	Ser	Tyr	Arg	Gly			
				85			90					95						
tgt	gta	gcc	cag	ctt	ttc	ata	ttt	ctg	gcc	ttg	ggg	gct	act	gaa	tat	336		
Cys	Val	Ala	Gln	Leu	Phe	Ile	Phe	Leu	Ala	Leu	Gly	Ala	Thr	Glu	Tyr			
100				105					110									



11/261

ctt ctc ctg gcc gtc atg tcc ttt gat agg ttt gta gct att tgt cgg 384  
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg  
 115 120 125

cct ctc cat tac tca gtt atc atg cac cag aga ctc tgc ctc cag ttg 432  
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu  
 130 135 140

gca gct gca tcc tgg gtt act ggt ttt agt aac tca gtg tgg ttg tct 480  
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser  
 145 150 155 160

acc ctg act ctc cag ctg cca ctc tgt gac ccc tat gtg ata gat cac 528  
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His  
 165 170 175

ttt ctc tgt gaa gtc cct gca ctg ctc aag tta tct tgt gtt gag aca 576  
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr  
 180 185 190

aca gca aat gag gct gaa cta ttc ctt gtc agt gag ctc ttc cat cta 624  
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu  
 195 200 205

ata ccc ctg aca ctc atc ctt ata tca tat gct ttt att gtc cga gca 672  
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala  
 210 215 220

gta ttg agg ata cag tct gct gaa ggt cga caa aaa gca ttt ggg aca 720  
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr  
 225 230 235 240

tgt ggt tcc cat cta att gtg gtg tct ctt ttt tat agt aca gcc gtc 768  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val  
 245 250 255

tct gtg tac ctg caa cca cct tcg ccc agc tcc aag gac caa gga aag 816  
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys  
 260 265 270

atg gtt tct ctc ttc tat gga atc att gca ccc atg ctg aat ccc ctt 864  
 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu  
 275 280 285

ata tat aca ctt agg aac aag gag gta aag gaa ggc ttt aaa agg ttg 912  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu  
 290 295 300

gtt gca aga agg aga tca tca agc cca aat 942  
 Val Ala Arg Arg Arg Ser Ser Ser Pro Asn  
 305 310

&lt;210&gt; 10

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly  
 1 5 10 15

Phe	Ser	Asp	Arg 20	Pro	Trp	Leu	Glu	Phe 25	Pro	Leu	Leu	Val	Val 30	Phe	Leu
Ile	Ser 35	Tyr	Thr	Val	Thr	Ile	Phe 40	Gly	Asn	Leu	Thr	Ile 45	Ile	Leu	Val
Ser	Arg 50	Leu	Asp	Thr	Lys	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Thr
Asn 65	Leu	Ser	Leu	Leu	Asp 70	Leu	Cys	Tyr	Thr	Thr 75	Cys	Thr	Val	Pro	Glu 80
Met	Leu	Val	Asn 85	Leu	Cys	Ser	Ile	Arg 90	Lys	Val	Ile	Ser	Tyr 95	Arg	Gly
Cys	Val	Ala	Gln 100	Leu	Phe	Ile	Phe	Leu 105	Ala	Leu	Gly	Ala	Thr 110	Glu	Tyr
Leu	Leu 115	Leu	Ala	Val	Met	Ser	Phe 120	Asp	Arg	Phe	Val	Ala 125	Ile	Cys	Arg
Pro 130	Leu	His	Tyr	Ser	Val	Ile 135	Met	His	Gln	Arg	Leu 140	Cys	Leu	Gln	Leu
Ala 145	Ala	Ala	Ser	Trp	Val 150	Thr	Gly	Phe	Ser	Asn 155	Ser	Val	Trp	Leu	Ser 160
Thr	Leu	Thr	Leu 165	Gln	Leu	Pro	Leu	Cys 170	Asp	Pro	Tyr	Val	Ile 175	Asp	His
Phe	Leu	Cys	Glu 180	Val	Pro	Ala	Leu	Leu 185	Lys	Leu	Ser	Cys	Val 190	Glu	Thr
Thr	Ala 195	Asn	Glu	Ala	Glu	Leu	Phe 200	Leu	Val	Ser	Glu	Leu 205	Phe	His	Leu
Ile	Pro 210	Leu	Thr	Leu	Ile	Leu 215	Ile	Ser	Tyr	Ala	Phé 220	Ile	Val	Arg	Ala
Val 225	Leu	Arg	Ile	Gln	Ser	Ala 230	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr 240
Cys	Gly	Ser	His 245	Leu	Ile	Val	Val	Ser	Leu 250	Phe	Tyr	Ser	Thr	Ala	Val
Ser	Val	Tyr 260	Leu	Gln	Pro	Pro	Ser	Pro 265	Ser	Ser	Lys	Asp	Gln 270	Gly	Lys
Met	Val 275	Ser	Leu	Phe	Tyr	Gly	Ile 280	Ile	Ala	Pro	Met	Leu 285	Asn	Pro	Leu
Ile	Tyr 290	Thr	Leu	Arg	Asn 295	Lys	Glu	Val	Lys	Glu	Gly 300	Phe	Lys	Arg	Leu
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<400> 11																
atg	gct	gct	gag	aat	tcc	tcc	ttc	gtg	aca	cag	ttt	atc	ctc	gca	ggc	48
Met	Ala	Ala	Glu	Asn	Ser	Ser	Phe	Val	Thr	Gln	Phe	Ile	Leu	Ala	Gly	
1				5					10					15		
tta	act	gac	caa	ccg	gga	gtc	cag	atc	ccc	ctc	ttc	ttc	ctg	ttt	cta	96
Leu	Thr	Asp	Gln	Pro	Gly	Val	Gln	Ile	Pro	Leu	Phe	Phe	Leu	Phe	Leu	
			20					25					30			
ggc	ttc	tac	gtg	gtc	act	gtg	gtg	ggg	aac	ctg	ggc	ttg	ata	acc	ctg	144
Gly	Phe	Tyr	Val	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Leu	Ile	Thr	Leu	
		35					40					45				

13/261

ata agg ctc aac tct cac ttg cac acc cct atg tac ttc ttc ctc tat	192
Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr	
50 55 60	
aac ttg tcc ttc ata gat ttc tgc tat tcc agt gtt atc act ccc aaa	240
Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys	
65 70 75 80	
atg ctg atg agc ttt gtc tta aag aag aac agc atc tcc tac gca ggg	288
Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly	
85 90 95	
tgt atg act cag ctc ttc ttc ttt ctt ttc ttt gtt gtc tct gag tcc	336
Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Glu Ser	
100 105 110	
ttc atc ctg tca gca atg gcg tat gac cgc tat gtg gcc atc tgt aac	384
Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn	
115 120 125	
cca ctg ttg tac atg gtc acc atg tct ccc cag gtg tgt ttt ctc ctt	432
Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu	
130 135 140	
ttg ttg ggt gtc tat ggg atg ggg ttt gct ggg gcc atg gcc cac aca	480
Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr	
145 150 155 160	
gct gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac att atc aac cat	528
Ala Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His	
165 170 175	
tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc tgc tcc aac aca	576
Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr	
180 185 190	
cac ctc aat gag ctt cta ctt ttt atc att gcg ggg ttt aac acc ttg	624
His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu	
195 200 205	
gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc atc ctc tac agc	672
Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser	
210 215 220	
atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa gct ttt gga aca	720
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr	
225 230 235 240	
tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt ggg tcc att acc	768
Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr	
245 250 255	
ttc atg tat ttc aag ccc cct tca agt aac tcc ctg gac cag gag aag	816
Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys	
260 265 270	
gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg ctg aac cct tta	864
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu	
275 280 285	

14/261

ata tac agt ctg agg aat aag gat gtg aag aaa gca tta agg aag gtc 912  
 ile tyr ser leu arg asn lys asp val lys lys ala leu arg lys val  
 290 295 300

tta tgt tgg aag ttc tgg cca ggg caa tca 942  
 leu cys trp lys phe trp pro gly gln ser  
 305 310

<210> 12  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Ala Ala Glu Asn Ser Ser Phe Val Thr Gln Phe Ile Leu Ala Gly  
 1 5 10 15  
 Leu Thr Asp Gln Pro Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu  
 20 25 30  
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Ser Glu Ser  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu  
 130 135 140  
 Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr  
 145 150 155 160  
 Ala Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His  
 165 170 175  
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr  
 180 185 190  
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu  
 195 200 205  
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser  
 210 215 220  
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr  
 245 250 255  
 Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys  
 260 265 270  
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val  
 290 295 300  
 Leu Cys Trp Lys Phe Trp Pro Gly Gln Ser  
 305 310

<210> 13  
 <211> 975  
 <212> DNA  
 <213> Homo sapiens

15/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(975)

&lt;400&gt; 13

atg gaa aaa aga aat cta aca gtt gtc agg gaa ttc gtc ctt ctg gga	48
Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly	
1 5 10 15	
ctt cct agc tca gca gag cag cag cac ctc ctg tct gtg ctc ttt ctc	96
Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu	
20 25 30	
tgt atg tat tta gcc acc acc ttg ggg aac atg ctc atc att gcg acg	144
Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr	
35 40 45	
att ggc ttt gac tct cac ctc cat tcc cct atg tac ttc ttc ctt agt	192
Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
aac ttg gcc ttt gtt gac atc tgc ttt acg tcg act aca gtc ccc caa	240
Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln	
65 70 75 80	
atg gta gtg aat atc ttg act ggc acc aag act atc tct ttt gca ggc	288
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly	
85 90 95	
tgc ctc acc cag ctc ttc ttc ttc gtt tct ttt gtg aat atg gac agc	336
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser	
100 105 110	
ctc ctt ctg tgt gtg atg gcg tat gat aga tat gtg gcg att tgc cac	384
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His	
115 120 125	
ccc tta cat tac acc gcc aga atg aac ctg tgc ctt tgt gtc cag cta	432
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu	
130 135 140	
gtg gct gga ctg tgg ctt gtt act tac ctc cac gcc ctc ctg cat act	480
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr	
145 150 155 160	
gtc cta ata gca cag ctg tcc ttc tgt gcc tcc aat atc atc cat cat	528
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His	
165 170 175	
ttc ttc tgt gat ctc aat cct ctc ctg cag ctc tct tgc tct gac atg	576
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Met	
180 185 190	
ccc ctc att atg caa ctg gct tgt gtg gat acc agc ctc aat gag atg	624
Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met	
195 200 205	
gag atg tac ctg gcc agc ttt gtc ttt gtt gtc ctg cct ctg ggg ctc	672
Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu	
210 215 220	

16/261

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atc ctg gtc tct tac ggc cac att gcc cgg gcc gtg ttg aag atc agg 720
Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile Arg
225                230                235                240

tca gca gaa ggg cgg aga aag gca ttc aac acc tgt tct tcc cac gtg 768
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His Val
                245                250                255

gct gtg gtg tct ctg ttt tac ggg agc atc atc ttc atg tat ctc cag 816
Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln
                260                265                270

cca gcc aag agc acc tcc cat gag cag gcc aag ttc ata gct ctg ttc 864
Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu Phe
                275                280                285

tac acc gta gtc act cct gcg ctg aac cca ctt att tac acc ctg agg 912
Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg
290                295                300

aac acg gag gtg aag agc gcc ctc cgg cac atg atg ggt aaa ttt gta 960
Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Met Gly Lys Phe Val
305                310                315                320

atc aca aaa ttg tgg 975
Ile Thr Lys Leu Trp
                325

```

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<210> 14
<211> 325
<212> PRT
<213> Homo sapiens

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<400> 14
Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu
20      25      30
Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr
35      40      45
Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser
50      55      60
Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln
65      70      75      80
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly
85      90      95
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser
100     105     110
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu
130     135     140
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr
145     150     155     160
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His
165     170     175
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Met
180     185     190
Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met
195     200     205

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17/261

Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu  
 210 215 220  
 Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile Arg  
 225 230 235 240  
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His Val  
 245 250 255  
 Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln  
 260 265 270  
 Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu Phe  
 275 280 285  
 Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 290 295 300  
 Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Met Gly Lys Phe Val  
 305 310 315 320  
 Ile Thr Lys Leu Trp  
 325

<210> 15  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 15  
 atg gaa gat aag aac cag aca gta gtg act gaa ttt ctc tta ttg ggc 48  
 Met Glu Asp Lys Asn Gln Thr Val Val Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 ctc aca gat cat ccc tat cag aag att gtt ctc ttc ttc atg ttt ctc 96  
 Leu Thr Asp His Pro Tyr Gln Lys Ile Val Leu Phe Phe Met Phe Leu  
 20 25 30  
 ttt gtt tat ctt atc acc ctg gga ggt aac ttg ggg atg atc act ctc 144  
 Phe Val Tyr Leu Ile Thr Leu Gly Gly Asn Leu Gly Met Ile Thr Leu  
 35 40 45  
 ata tgg att gat ccc aga ctc cac act cct atg tac ttt ttt ctt agg 192  
 Ile Trp Ile Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 cac ttc cac ctg tcc ttt gtg gac acc tgc ttc tcc tca gtt gtg agc 240  
 His Phe His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser  
 65 70 75 80  
 ccc aag atg ctc act gac ttc ttt gtg aag agg aaa gcc att tct ttc 288  
 Pro Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe  
 85 90 95  
 ctt ggc tgt gct ttg cag cag tgg ttc ttt ggg ttc ttt gtg gca gca 336  
 Leu Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala  
 100 105 110  
 gac tgt ttc ctc ttg gag tcc atg gcc tat gac tgc tat gtg gcc atc 384  
 Asp Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile  
 115 120 125

18/261

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tgt aac cca ttg tta tac tca gtt gct atg tcc cag agg ctc tgc atc 432
Cys Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile
    130                      135                      140

cag cta gtg gtg ggt ccc tat gtc att gga ctc atg aat acc atg act 480
Gln Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr
    145                      150                      155                      160

cac aca aca aat gca ttt tgt ctc cct ttt tgt ggc cct aat gtc atc 528
His Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile
                      165                      170                      175

aat cct ttc ttc tgt gat atg tcc ccc tta ctt tcc ctt gta tgt gct 576
Asn Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala
                      180                      185                      190

gat acc agg ctc aat aag ttg gca gtt ttc atc gtg gct gga gct gtg 624
Asp Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val
                      195                      200                      205

gga gtc ttc agt ggt ctg act atc ctg att tcc tac att tac atc ctc 672
Gly Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu
    210                      215                      220

atg gcc atc ctg agg atc cgc tct gct gat ggg agg tgc aaa acc ttt 720
Met Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe
    225                      230                      235                      240

tct act tgc tct tct cac ctg aca gct gtt ttc atc tcg tat ggt acc 768
Ser Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr
                      245                      250                      255

ctt ttc ttt att tat gta cat ccc agt gca acc ttc tcc ctg gat ctc 816
Leu Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu
                      260                      265                      270

aat aaa gta gtg tct gtg ttt tac aca gca gtg att cct atg ttg aac 864
Asn Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn
    275                      280                      285

cca ctt atc tac agc ttg aga aac aag gaa gtc aaa gat gcc atc cac 912
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His
    290                      295                      300

agg act gtc act cag agg aag ttt tgc aag gcc 945
Arg Thr Val Thr Gln Arg Lys Phe Cys Lys Ala
    305                      310                      315

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&lt;210&gt; 16

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Met Glu Asp Lys Asn Gln Thr Val Val Thr Glu Phe Leu Leu Leu Gly
 1          5          10          15
Leu Thr Asp His Pro Tyr Gln Lys Ile Val Leu Phe Phe Met Phe Leu
    20          25          30
Phe Val Tyr Leu Ile Thr Leu Gly Gly Asn Leu Gly Met Ile Thr Leu
    35          40          45

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19/261

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Ile Trp Ile Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50      55      60
His Phe His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser
 65      70      75      80
Pro Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe
      85      90      95
Leu Gly Cys Ala Leu Gln Gln Trp Phe Gly Phe Phe Val Ala Ala
      100      105      110
Asp Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile
      130      135      140
Gln Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr
 145      150      155      160
His Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile
      165      170      175
Asn Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala
      180      185      190
Asp Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val
      195      200      205
Gly Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu
      210      215      220
Met Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe
 225      230      235      240
Ser Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr
      245      250      255
Leu Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu
      260      265      270
Asn Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His
      290      295      300
Arg Thr Val Thr Gln Arg Lys Phe Cys Lys Ala
 305      310      315

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<210> 17  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

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<400> 17
atg aag aga aag aac ttc aca gaa gtg tca gaa ttc att ttc ttg gga 48
Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1      5      10      15

ttt tct agc ttt gga aag cat cag ata acc ctc ttt gtg gtt ttc cta 96
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
      20      25      30

act gtc tac att tta act ctg gtt gct aac atc atc att gtg act atc 144
Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
      35      40      45

atc tgc att gac cat cat ctc cac act ccc atg tat ttc ttc cta agc 192
Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60

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20/261

atg	ctg	gct	agt	tca	gag	acg	gtg	tac	aca	ctg	gtc	att	gtg	cca	cga	240
Met	Leu	Ala	Ser	Ser	Glu	Thr	Val	Tyr	Thr	Leu	Val	Ile	Val	Pro	Arg	
65					70					75					80	
atg	ctt	ttg	agc	ctc	att	ttt	cat	aac	caa	cct	atc	tcc	ttg	gca	ggc	288
Met	Leu	Leu	Ser	Leu	Ile	Phe	His	Asn	Gln	Pro	Ile	Ser	Leu	Ala	Gly	
				85					90					95		
tgt	gct	aca	caa	atg	ttc	ttt	ttt	gtt	atc	ttg	gcc	act	aat	aat	tgc	336
Cys	Ala	Thr	Gln	Met	Phe	Phe	Phe	Val	Ile	Leu	Ala	Thr	Asn	Asn	Cys	
			100					105					110			
ttc	ctg	ctt	act	gca	atg	ggg	tat	gac	cgc	tat	gtg	gcc	atc	tgc	aga	384
Phe	Leu	Leu	Thr	Ala	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Arg	
		115					120					125				
ccc	ctg	aga	tac	act	gtc	atc	atg	agc	aag	gga	cta	tgt	gcc	cag	ctg	432
Pro	Leu	Arg	Tyr	Thr	Val	Ile	Met	Ser	Lys	Gly	Leu	Cys	Ala	Gln	Leu	
		130				135					140					
gtg	tgt	ggg	tcc	ttt	ggc	att	ggt	ctg	act	atg	gca	gtt	ctc	cat	gtg	480
Val	Cys	Gly	Ser	Phe	Gly	Ile	Gly	Leu	Thr	Met	Ala	Val	Leu	His	Val	
145					150					155					160	
aca	gcc	atg	ttc	aat	ttg	ccg	ttc	tgt	ggc	aca	gtg	gta	gac	cac	ttc	528
Thr	Ala	Met	Phe	Asn	Leu	Pro	Phe	Cys	Gly	Thr	Val	Val	Asp	His	Phe	
				165					170					175		
ttt	tgt	gac	att	tac	cca	gtc	atg	aaa	ctt	tct	tgc	att	gat	acc	act	576
Phe	Cys	Asp	Ile	Tyr	Pro	Val	Met	Lys	Leu	Ser	Cys	Ile	Asp	Thr	Thr	
			180					185					190			
atc	aat	gag	ata	ata	aat	tat	ggt	gta	agt	tca	ttt	gtg	att	ttt	gtg	624
Ile	Asn	Glu	Ile	Ile	Asn	Tyr	Gly	Val	Ser	Ser	Phe	Val	Ile	Phe	Val	
		195					200					205				
ccc	ata	ggc	ctg	ata	ttt	atc	tcc	tat	gtc	ctt	gtc	atc	tct	tcc	atc	672
Pro	Ile	Gly	Leu	Ile	Phe	Ile	Ser	Tyr	Val	Leu	Val	Ile	Ser	Ser	Ile	
		210				215					220					
ctt	caa	att	gcc	tca	gct	gag	ggc	cgg	aag	aag	acc	ttt	gcc	acc	tgt	720
Leu	Gln	Ile	Ala	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Thr	Phe	Ala	Thr	Cys	
225					230					235					240	
gtc	tcc	cac	ctc	act	gtg	gtt	att	gtc	cac	tgt	ggc	tgt	gcc	tcc	att	768
Val	Ser	His	Leu	Thr	Val	Val	Ile	Val	His	Cys	Gly	Cys	Ala	Ser	Ile	
				245					250					255		
gcc	tac	ctc	aag	ccg	aag	tca	gaa	agt	tca	ata	gaa	aaa	gac	ctt	gtt	816
Ala	Tyr	Leu	Lys	Pro	Lys	Ser	Glu	Ser	Ser	Ile	Glu	Lys	Asp	Leu	Val	
			260					265					270			
ctc	tca	gtg	acg	tac	acc	atc	atc	act	ccc	ttg	ctg	aac	cct	gtt	gtt	864
Leu	Ser	Val	Thr	Tyr	Thr	Ile	Ile	Thr	Pro	Leu	Leu	Asn	Pro	Val	Val	
		275					280					285				
tac	agt	ctg	aga	aac	aag	gag	gta	aag	gat	gcc	cta	tgc	aga	gtt	ctc	912
Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Asp	Ala	Leu	Cys	Arg	Val	Leu	
		290				295					300					

21/261

tgt ctg cac aag att att acc agc tgg  
 Cys Leu His Lys Ile Ile Thr Ser Trp  
 305 310

939

<210> 18  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu  
 20 25 30  
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile  
 35 40 45  
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg  
 65 70 75 80  
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly  
 85 90 95  
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys  
 100 105 110  
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu  
 130 135 140  
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val  
 145 150 155 160  
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe  
 165 170 175  
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr  
 180 185 190  
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val  
 195 200 205  
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile  
 210 215 220  
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys  
 225 230 235 240  
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile  
 245 250 255  
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val  
 260 265 270  
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu  
 290 295 300  
 Cys Leu His Lys Ile Ile Thr Ser Trp  
 305 310

<210> 19  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

22/261

<400> 19  
 atg gct gca gga aat cac tct aca gtg aca gag ttc att ctc aag ggt 48  
 Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly  
 1 5 10 15

tta acg aag aga gca gac ctc cag ctc ccc ctc ttt ctc ctc ttc ctc 96  
 Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30

ggg atc tac ttg gtc acc atc gtg ggg aac ctg ggc atg atc act cta 144  
 Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu  
 35 40 45

att tgt ctg aac tct cag ctg cac acc ccc atg tac tac ttt ctc agc 192  
 Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60

aat ctg tca ctc atg gat ctc tgc tac tcc tcc gtc att acc cct aag 240  
 Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80

atg ctg gtg aac ttt gtg tca gag aaa aac atc atc tcc tac gca ggg 288  
 Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly  
 85 90 95

tgc atg tca cag ctc tac ttc ttc ctt gtt ttt gtc att gct gag tgt 336  
 Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys  
 100 105 110

tac atg ctg aca gtg atg gcc tac gac cgc tat gtt gcc atc tgc cac 384  
 Tyr Met Leu Thr Val Met Ala Thr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125

cct ttg ctt tac aac atc att atg tct cat cac acc tgc ctg ctg ctg 432  
 Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu  
 130 135 140

gtg gct gtg gtc tac gcc atc gga ctc att ggc tcc aca ata gaa act 480  
 Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr  
 145 150 155 160

ggc ctc atg tta aaa ctg ccc tat tgt gag cac ctc atc agt cac tac 528  
 Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr  
 165 170 175

ttc tgt gac atc ctc cct ctc atg aag ctg tcc tgc tct agc acc tat 576  
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190

gat gtt gag atg aca gtc ttc ttt tgc gct gga ttc aac atc ata gtc 624  
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val  
 195 200 205

acg agc tta aca gtt ctt gtt tct tac acc ttc att ctc tcc agc atc 672  
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile  
 210 215 220

ctc ggc atc agc acc aca gag ggg aga tcc aaa gcc ttc agc acc tgc 720  
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys  
 225 230 235 240

23/261

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agc tcc cac ctt gca gcc gtg gga atg ttc tat gga tca act gca ttc 768
Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
                245                250                255

atg tac tta aaa ccc tcc aca atc agt tcc ttg acc cag gag aat gtg 816
Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
                260                265                270

gcc tct gtg ttc tac acc acg gta atc ccc atg ttg aat ccc cta atc 864
Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
                275                280                285

tac agc ctg agg aac aag gaa gta aag gct gcc gtg cag aaa acg ctg 912
Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
                290                295                300

agg ggt aaa ctc att cat cat agg tgg 939
Arg Gly Lys Leu Ile His His Arg Trp
305                310

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<210> 20  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 20

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Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
 1      5      10      15
Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20      25      30
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
      35      40      45
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
      50      55      60
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
      65      70      75      80
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
      85      90      95
Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
      100     105     110
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115     120     125
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
      130     135     140
Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
      145     150     155     160
Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
      165     170     175
Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
      180     185     190
Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
      195     200     205
Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
      210     215     220
Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
      225     230     235     240
Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
      245     250     255
Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
      260     265     270

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24/261

Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu  
                   290                  295                  300  
 Arg Gly Lys Leu Ile His His Arg Trp  
 305                  310

<210> 21  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(948)

<400> 21  
 atg gag agc gga aac caa tca aca gtg act gaa ttt atc ttc act gga 48  
 Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly  
   1                  5                  10                  15  
 ttc cct cag ctt cag gat gcc ttc cag ctt ctc ttt ttc tcc att ttc 96  
 Phe Pro Gln Leu Gln Asp Ala Phe Gln Leu Leu Phe Phe Ser Ile Phe  
                   20                  25                  30  
 ctg gca acc tat ctg ctg aca ctg ctg gag aat ctt ctt atc atc tta 144  
 Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 gct atc cac agt gat ggg cag ctg cat aag ccc atg tac ttc ttc ttg 192  
 Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met Tyr Phe Phe Leu  
                   50                  55                  60  
 agc cac ctc tcc ttc ctg gag atg tgg tat gtc aca gtc atc agc ccc 240  
 Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr Val Ile Ser Pro  
                   65                  70                  75                  80  
 aag atg ctt gtt gac ttc ctc agt cat gac aag agt att tcc ttc aat 288  
 Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser Ile Ser Phe Asn  
                   85                  90                  95  
 ggc tgc atg act caa ctt tac ttt ttt gtg acc ttt gtc tgc act gag 336  
 Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe Val Cys Thr Glu  
                   100                  105                  110  
 tac atc ctt ctt gct atc atg gcc ttt gac cgc tat gta gcc att tgt 384  
 Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
                   115                  120                  125  
 aat cca cta cgc tac cca gtc atc atg acc aac cag ctc tgt ggc aca 432  
 Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln Leu Cys Gly Thr  
                   130                  135                  140  
 ctg gct gga gga tgc tgg ttc tgt gga ctc atg act gcc atg att aag 480  
 Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr Ala Met Ile Lys  
                   145                  150                  155                  160  
 atg gtt ttt ata gca caa ctt cac tac tgt ggc atg cct cag atc aat 528  
 Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met Pro Gln Ile Asn  
                   165                  170                  175

25/261

cac tac ttt tgt gat atc tct cca ctc ctt aac gtc tcc tgt gag gat 576  
 His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val Ser Cys Glu Asp  
 180 185 190

gcc tca cag gct gag atg atg gtc atc ttt ttc ctc agc att ctg gta 624  
 Ala Ser Gln Ala Glu Met Met Val Ile Phe Phe Leu Ser Ile Leu Val  
 195 200 205

ttg ctg gtt ccc ctt gtg ttg ata ttc atc tcc tac atc ttc ata gtt 672  
 Leu Leu Val Pro Leu Val Leu Ile Phe Ile Ser Tyr Ile Phe Ile Val  
 210 215 220

tcc acc atc ctc aag atc tcc tca gtg gaa gga cag tgc aaa gcc ttc 720  
 Ser Thr Ile Leu Lys Ile Ser Ser Val Glu Gly Gln Cys Lys Ala Phe  
 225 230 235 240

gcc acc tgt gct tcc cac ctc aca gtg gtc gtc gtc cac tat ggc tgt 768  
 Ala Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Cys  
 245 250 255

gct tcc ttt atc tac ttg agg ccc aca tcc ctg tac tct tca gat aag 816  
 Ala Ser Phe Ile Tyr Leu Arg Pro Thr Ser Leu Tyr Ser Ser Asp Lys  
 260 265 270

gac cgg ctc gtg gca gtg act tat act gtg att act cca cta ctc aac 864  
 Asp Arg Leu Val Ala Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn  
 275 280 285

ccc ctt gtc tat aca ctg aga aat aaa gaa gta aag atg gct ctg aga 912  
 Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Met Ala Leu Arg  
 290 295 300

aag gtt ctg ggt aga tgc tta aat tcc aaa act gta 948  
 Lys Val Leu Gly Arg Cys Leu Asn Ser Lys Thr Val  
 305 310 315

<210> 22  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly  
 1 5 10 15  
 Phe Pro Gln Leu Gln Asp Ala Phe Gln Leu Leu Phe Phe Ser Ile Phe  
 20 25 30  
 Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr Val Ile Ser Pro  
 65 70 75 80  
 Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser Ile Ser Phe Asn  
 85 90 95  
 Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe Val Cys Thr Glu  
 100 105 110  
 Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln Leu Cys Gly Thr  
 130 135 140

26/261

Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr Ala Met Ile Lys  
 145 150 155 160  
 Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met Pro Gln Ile Asn  
 165 170 175  
 His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val Ser Cys Glu Asp  
 180 185 190  
 Ala Ser Gln Ala Glu Met Met Val Ile Phe Phe Leu Ser Ile Leu Val  
 195 200 205  
 Leu Leu Val Pro Leu Val Leu Ile Phe Ile Ser Tyr Ile Phe Ile Val  
 210 215 220  
 Ser Thr Ile Leu Lys Ile Ser Ser Val Glu Gly Gln Cys Lys Ala Phe  
 225 230 235 240  
 Ala Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Cys  
 245 250 255  
 Ala Ser Phe Ile Tyr Leu Arg Pro Thr Ser Leu Tyr Ser Ser Asp Lys  
 260 265 270  
 Asp Arg Leu Val Ala Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn  
 275 280 285  
 Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Met Ala Leu Arg  
 290 295 300  
 Lys Val Leu Gly Arg Cys Leu Asn Ser Lys Thr Val  
 305 310 315

<210> 23  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (939)

<400> 23  
 atg gga gac aat ata aca tcc atc aga gag ttc ctc cta ctg gga ttt 48  
 Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe  
 1 5 10 15  
 ccc gtt ggc cca agg att cag atg ctc ctc ttt ggg ctc ttc tcc ctg 96  
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20 25 30  
 ttc tac gtc ttc acc ctg ctg ggg aac ggg acc ata ctg ggg ctc atc 144  
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile  
 35 40 45  
 tca ctg gac tcc aga ctg cac gcc ccc atg tac ttc ttc ctc tca cac 192  
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His  
 50 55 60  
 ctg gcg gtc gtc gac atc gcc tac gcc tgc aac acg gtg ccc egg atg 240  
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met  
 65 70 75 80  
 ctg gtg aac ctc ctg cat cca gcc aag ccc atc tcc ttt gcg ggc cgc 288  
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg  
 85 90 95  
 atg atg cag acc ttt ctg ttt tcc act ttt gct gtc aca gaa tgt ctc 336  
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu  
 100 105 110



27/261

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ctc ctg gtg gtg atg tcc tat gat ctg tac gtg gcc atc tgc cac ccc 384
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115                      120                      125

ctc cga tat ttg gcc atc atg acc tgg aga gtc tgc atc acc ctc gcg 432
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130                      135                      140

gtg act tcc tgg acc act gga gtc ctt tta tcc ttg att cat ctt gtg 480
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145                      150                      155                      160

tta ctt cta cct tta ccc ttc tgt agg ccc cag aaa att tat cac ttt 528
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165                      170                      175

ttt tgt gaa atc ttg gct gtt ctc aaa ctt gcc tgt gca gat acc cac 576
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180                      185                      190

atc aat gag aac atg gtc ttg gcc gga gca att tct ggg ctg gtg gga 624
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195                      200                      205

ccc ttg tcc aca att gta gtt tca tat atg tgc atc ctc tgt gct atc 672
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210                      215                      220

ctt cag atc caa tca agg gaa gtt cag agg aaa gcc ttc cgc acc tgc 720
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
      225                      230                      235                      240

ttc tcc cac ctc tgt gtg att gga ctc gtt tat ggc aca gcc att atc 768
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
      245                      250                      255

atg tat gtt gga ccc aga tat ggg aac ccc aag gag cag aag aaa tat 816
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260                      265                      270

ctc ctg ctg ttt cac agc ctc ttt aat ccc atg ctc aat ccc ctt atc 864
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275                      280                      285

tgt agt ctt agg aac tca gaa gtg aag aat act ttg aag aga gtg ctg 912
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290                      295                      300

gga agg agc caa tgg tgt aag tcc cag 939
Gly Arg Ser Gln Trp Cys Lys Ser Gln
      305                      310

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&lt;210&gt; 24

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
  1                      5                      10                      15

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28/261

Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20 25 30  
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile  
 35 40 45  
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His  
 50 55 60  
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met  
 65 70 75 80  
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg  
 85 90 95  
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu  
 100 105 110  
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro  
 115 120 125  
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala  
 130 135 140  
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val  
 145 150 155 160  
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe  
 165 170 175  
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His  
 180 185 190  
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly  
 195 200 205  
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile  
 210 215 220  
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys  
 225 230 235 240  
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile  
 245 250 255  
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Tyr  
 260 265 270  
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu  
 290 295 300  
 Gly Arg Ser Gln Trp Cys Lys Ser Gln  
 305 310

&lt;210&gt; 25

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(960)

&lt;400&gt; 25

atg gaa tgg gaa aac caa acc att ctg gtg gaa ttt ttt ctg aag gga 48  
 Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly  
 1 5 10 15  
 cat tct gtt cac cca agg ctt gag tta ctc ttt ttt gtg cta atc ttc 96  
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe  
 20 25 30  
 ata atg tat gtg gtc atc ctt ctg ggg aat ggt act ctc att tta atc 144  
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile  
 35 40 45

29/261

agc atc ttg gac cct cac ctt cac acc cct atg tac ttc ttt ctg ggg	192
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly	
50 55 60	
aac ctc tcc ttc ttg gac atc tgc tac acc acc acc tct att ccc tcc	240
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser	
65 70 75 80	
aca cta gtg agc ttc ctt tca gaa aga aag acc att tcc ttt tct ggc	288
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly	
85 90 95	
tgt gca gtg cag atg ttc ctt ggc ttg gcc atg ggg aca aca gag tgt	336
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys	
100 105 110	
gtg ctt ctg ggc atg atg gcc ttt gac cgc tat gtg gct atc tgc aac	384
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn	
115 120 125	
cct ctg aga tat ccc atc atc atg agc aag aat gcc tat gta ccc atg	432
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met	
130 135 140	
gct gtt ggg tcc tgg ttt gca ggg att gtc aac tct gca gta caa act	480
Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr	
145 150 155 160	
aca ttt gta gta caa ttg cct ttc tgc agg aag aat gtc atc aat cat	528
Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His	
165 170 175	
ttc tca tgt gaa att cta gct gtc atg aag ttg gcc tgt gct gac atc	576
Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile	
180 185 190	
tca ggc aat gag ttc ctc atg ctt gtg gcc aca ata ttg ttc aca ttg	624
Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu	
195 200 205	
atg cca ctg ctc ttg ata gtt atc tct tac tca tta atc att tcc agc	672
Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser	
210 215 220	
atc ctc aag att cac tcc tct gag ggg aga agc aaa gct ttc tct acc	720
Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr	
225 230 235 240	
tgc tca gcc cat ctg act gtg gtc ata ata ttc tat ggg acc atc ctc	768
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu	
245 250 255	
ttc atg tat atg aag ccc aag tct aaa gag aca ctt aat tca gat gac	816
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp	
260 265 270	
ttg gat gct acc gac aaa att ata tcc atg ttc tat ggg gtg atg act	864
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr	
275 280 285	

30/261

ccc atg atg aat cct tta atc tac agt ctt aga aac aag gat gtg aaa 912  
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 290 295 300

gag gca ctc tgc agg ctg ttc agg agt gga ttt cat tcc cag tac aac 960  
 Glu Ala Leu Cys Arg Leu Phe Arg Ser Gly Phe His Ser Gln Tyr Asn  
 305 310 315 320

&lt;210&gt; 26

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly  
 1 5 10 15  
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe  
 20 25 30  
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile  
 35 40 45  
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ile Pro Ser  
 65 70 75 80  
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys  
 100 105 110  
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met  
 130 135 140  
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr  
 145 150 155 160  
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His  
 165 170 175  
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile  
 180 185 190  
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu  
 195 200 205  
 Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser  
 210 215 220  
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu  
 245 250 255  
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp  
 260 265 270  
 Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr  
 275 280 285  
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 290 295 300  
 Glu Ala Leu Cys Arg Leu Phe Arg Ser Gly Phe His Ser Gln Tyr Asn  
 305 310 315 320

&lt;210&gt; 27

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

31/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(930)

&lt;400&gt; 27

aat cat tct cgg gtg aca gaa ttt gtg ttg ctg gga ctg tct agt tca	48
Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly Leu Ser Ser Ser	
1 5 10 15	
agg gag ctc caa cct ttc ttg ttt ctt aca ttt tca cta ctt tat cta	96
Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser Leu Leu Tyr Leu	
20 25 30	
gca att ctg ttg ggc aac ttt ctc atc atc ctc act gtg acc tca gat	144
Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr Val Thr Ser Asp	
35 40 45	
tcc cgc ctt cac acc ccc atg tac ttt ctg ctt gca aac ctg tca ttt	192
Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Phe	
50 55 60	
ata gac atc tgg tac att tcc tcc act gtc cca aac atg cta gtc aat	240
Ile Asp Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn	
65 70 75 80	
atc ctc tct gag att aaa acc atc tcc ttc tct ggt tgc ttc ctg caa	288
Ile Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln	
85 90 95	
ttc tat ttc ttt ttt tca ctg ggt aca aca gag tgt ttc ttt tta tca	336
Phe Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser	
100 105 110	
gtt atg gct tat gat cgg tac ctg gcc atc tgt cgt cca tta cac tac	384
Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr	
115 120 125	
ccc tcc atc atg act ggg aag ttc tgt ata att ctg gtc tgt gta tgc	432
Pro Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys	
130 135 140	
tgg gta ggc gga ttt ctc tgc tat cca gtc cct att gtt ctt atc tcc	480
Trp Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser	
145 150 155 160	
caa ctt ccc ttc tgt ggg ccc aac atc att gac cac ttg gtg tgt gac	528
Gln Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp	
165 170 175	
cca ggc cca ttg ttt gca ctg gcc tgc atc tct gct cct tcc act gag	576
Pro Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu	
180 185 190	
ctt atc tgt tac acc ttc aac tcg atg att atc ttt ggg ccc ttc ctc	624
Leu Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu	
195 200 205	
tcc atc ttg gga tct tac act ctg gtc atc aga gct gtg ctt tgt att	672
Ser Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile	
210 215 220	

32/261

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ccc tct ggt gct ggt cga act aaa gct ttc tcc aca tgt ggg tcc cac 720
Pro Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His
225                230                235                240

cta atg gtg gtg tct cta ttc tat gga acc ctt atg gtg atg tat gtg 768
Leu Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val
                245                250                255

agc cca aca tca ggg aac cca gca gga atg cag aag atc atc act ctg 816
Ser Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu
                260                265                270

gta tac aca gca atg act cca ttc tta aat ccc ctt atc tat agt ctt 864
Val Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu
                275                280                285

cga aac aaa gac atg aaa gat gct cta aag aga gtc ctg ggc agg aga 912
Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Arg Arg
290                295                300

cag tgg cct tcc tct atc
Gln Trp Pro Ser Ser Ile
305                310

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<210> 28  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

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<400> 28
Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly Leu Ser Ser Ser
1          5          10          15
Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser Leu Leu Tyr Leu
20          25          30
Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr Val Thr Ser Asp
35          40          45
Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Phe
50          55          60
Ile Asp Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn
65          70          75          80
Ile Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln
85          90          95
Phe Tyr Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser
100         105         110
Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr
115         120         125
Pro Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys
130         135         140
Trp Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser
145         150         155         160
Gln Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp
165         170         175
Pro Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu
180         185         190
Leu Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu
195         200         205
Ser Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile
210         215         220
Pro Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His
225         230         235         240

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[illegible]

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<220>
<221> CDS .
<222> (1) ... (942)
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BNSDOCID: <WO 03000735A2 | >

34/261

tcc ttg att tca cgc ctc cca ttc tgt ggc ccc aat cgc att cag cac 528  
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His  
 165 170 175

gtc ttt tgt gac ttc cct cct gtg ctg agt ttg gct tgc act gat acg 576  
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190

tct aca aat gtc cta gta gat ttt gtt ata aat tcc tgc aag atc cta 624  
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu  
 195 200 205

gcc acc ttc ctg ctg atc ctc tgc tcc tat gtg cag atc atc tgc aca 672  
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr  
 210 215 220

gtg ctc aga att ccc tca gct gcc ggc aag agg aag gcc atc tcc acg 720  
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr  
 225 230 235 240

tgt gcc tcc cac ctc act gtg gtt ctc atc ttc tat ggg agc atc ctt 768  
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu  
 245 250 255

tcc atg tat gtg cgg ctg aag aag agc tac tca ctg gac tat gac cag 816  
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln  
 260 265 270

gcc ctg gca gtg gtc tac tca gtg ctc aca ccc ttc ctc aac ccc ttc 864  
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe  
 275 280 285

atc tac agc ttg cac aac aag gag atc aag gag gct tgg aaa aag tac 912  
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr  
 290 295 300

atc tgc agg agg cag cca gcc acg gaa atg 942  
 Ile Cys Arg Arg Gln Pro Ala Thr Glu Met  
 305 310

<210> 30  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu  
 20 25 30  
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val  
 35 40 45  
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys  
 100 105 110



35/261

Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
           115                  120          125  
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile  
       130                  135          140  
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile  
 145                  150          155          160  
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His  
           165                  170          175  
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
           180                  185          190  
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu  
           195                  200          205  
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr  
       210                  215          220  
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr  
 225                  230          235          240  
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu  
           245                  250          255  
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln  
           260                  265          270  
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe  
       275                  280          285  
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr  
       290                  295          300  
 Ile Cys Arg Arg Gln Pro Ala Thr Glu Met  
 305                  310

<210> 31  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 31  
 atg gga agt ttc aac acc agt ttt gaa gat ggc ttc att ttg gtg gga 48  
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly  
   1                  5                  10                  15  
  
 ttc tca gat tgg ccg caa ctg gag ccc atc ctg ttt gtc ttt att ttt 96  
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe  
           20                  25                  30  
  
 att ttc tac tcc cta act ctc ttt ggc aac acc atc atc atc gct ctc 144  
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu  
           35                  40                  45  
  
 tcc tgg cta gac ctt cgg ctg cac aca cct atg tac ttc ttt ctc tct 192  
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
       50                  55                  60  
  
 cat ctg tcc ctc ctg gac ctc tgc ttc acc acc agc acc gtg ccc cag 240  
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln  
       65                  70                  75                  80  
  
 ctc ctg atc aac ctt tgc ggg gtg gac cgc acc atc acc cgt gga ggg 288  
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly  
           85                  90                  95

36/261

tgt	gtg	gct	cag	ctc	ttc	atc	tac	cta	gcc	ctg	ggc	tcc	aca	gag	tgt	336
Cys	Val	Ala	Gln	Leu	Phe	Ile	Tyr	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	
		100						105					110			
gtg	ctc	ctg	gtg	gtg	atg	gcc	ttt	gac	cgc	tat	gct	gct	gtc	tgt	cgt	384
Val	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg	
		115					120					125				
cca	ctc	cac	tac	atg	gcc	atc	atg	cac	ccc	cat	ctc	tgc	cag	acc	ctg	432
Pro	Leu	His	Tyr	Met	Ala	Ile	Met	His	Pro	His	Leu	Cys	Gln	Thr	Leu	
		130				135					140					
gct	atc	gcc	tcc	tgg	ggg	gcg	ggg	ttc	gtg	aac	tct	ctg	atc	cag	aca	480
Ala	Ile	Ala	Ser	Trp	Gly	Ala	Gly	Phe	Val	Asn	Ser	Leu	Ile	Gln	Thr	
145					150					155					160	
ggg	ctc	gca	atg	gcc	atg	cct	ctc	tgt	ggc	cat	cga	ctg	aat	cac	ttc	528
Gly	Leu	Ala	Met	Ala	Met	Pro	Leu	Cys	Gly	His	Arg	Leu	Asn	His	Phe	
			165					170						175		
ttc	tgt	gag	atg	cct	gta	ttt	ctg	aag	ttg	gct	tgt	gcg	gac	aca	gaa	576
Phe	Cys	Glu	Met	Pro	Val	Phe	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	Glu	
			180					185					190			
gga	aca	gag	gcc	aag	atg	ttt	gtg	gcc	cga	gtc	ata	gtc	gtg	gct	gtt	624
Gly	Thr	Glu	Ala	Lys	Met	Phe	Val	Ala	Arg	Val	Ile	Val	Val	Ala	Val	
		195					200					205				
cct	gca	gca	ctt	att	cta	ggc	tcc	tat	gtg	cac	att	gct	cat	gca	gtg	672
Pro	Ala	Ala	Leu	Ile	Leu	Gly	Ser	Tyr	Val	His	Ile	Ala	His	Ala	Val	
		210				215					220					
ctg	agg	gtg	aag	tca	acg	gct	ggg	cgc	aga	aag	gct	ttt	ggg	act	tgt	720
Leu	Arg	Val	Lys	Ser	Thr	Ala	Gly	Arg	Arg	Lys	Ala	Phe	Gly	Thr	Cys	
225					230					235					240	
ggg	tcc	cac	ctc	cta	gta	gtt	ttc	ctt	ttt	tat	ggc	tca	gcc	atc	tac	768
Gly	Ser	His	Leu	Leu	Val	Val	Phe	Leu	Phe	Tyr	Gly	Ser	Ala	Ile	Tyr	
			245					250						255		
aca	tat	ctc	caa	tcc	atc	cac	aat	tat	tct	gag	cgt	gag	gga	aaa	ttt	816
Thr	Tyr	Leu	Gln	Ser	Ile	His	Asn	Tyr	Ser	Glu	Arg	Glu	Gly	Lys	Phe	
			260					265					270			
gtt	gcc	ctt	ttt	tat	act	ata	att	acc	ccc	att	ctc	aat	cct	ctc	att	864
Val	Ala	Leu	Phe	Tyr	Thr	Ile	Ile	Thr	Pro	Ile	Leu	Asn	Pro	Leu	Ile	
		275					280					285				
tat	aca	cta	aga	aac	aag	gac	gtg	aag	ggg	gct	ctg	tgg	aaa	gta	cta	912
Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly	Ala	Leu	Trp	Lys	Val	Leu	
		290				295					300					
tgg	agg	ggc	agg	gac	tca	ggg	cag	tgg								939
Trp	Arg	Gly	Arg	Asp	Ser	Gly	Gln	Trp								
305					310											

&lt;210&gt; 32

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

37/261

&lt;400&gt; 32

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Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1      5      10      15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20      25      30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
 35      40      45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65      70      75      80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
 85      90      95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
 100     105     110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
 115     120     125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
 130     135     140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
 145     150     155     160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
 165     170     175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
 180     185     190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
 195     200     205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
 210     215     220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
 225     230     235     240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
 245     250     255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
 260     265     270
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
 275     280     285
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
 290     295     300
Trp Arg Gly Arg Asp Ser Gly Gln Trp
 305     310

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&lt;210&gt; 33

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(942)

&lt;400&gt; 33

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atg aaa ggg gca aac ctg agc caa ggg atg gag ttt gag ctc ttg ggc 48
Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1      5      10      15

ctc acc act gac ccc cag ctc cag agg ctg ctc ttc gtg gtg ttc ctg 96
Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
 20      25      30

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38/261

ggc atg tac aca gcc act ctg ctg ggg aac ctg gtc atg ttc ctc ctg	144
Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu	
35 40 45	
atc cat gtg agt gcc acc ctg cac aca ccc atg tac tcc ctc ctg aag	192
Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys	
50 55 60	
agc ctc tcc ttc ttg gat ttc tgc tac tcc tcc acg gtt gtg ccc cag	240
Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln	
65 70 75 80	
acc ctg gtg aac ttc ttg gcc aag agg aaa gtg atc tct tat ttt ggc	288
Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly	
85 90 95	
tgc atg act cag atg ttc ttc tat gcg ggt ttt gcc acc agt gag tgc	336
Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys	
100 105 110	
tat ctc atc gct gcc atg gcc tat gac cgc tat gcc gct att tgt aac	384
Tyr Leu Ile Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn	
115 120 125	
ccc ctg ctc tac tca acc atc atg tct cct gag gtc tgt gcc tcg ctg	432
Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu	
130 135 140	
att gtg ggc tcc tac agt gca gga ttc ctc aat tct ctt atc cac act	480
Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr	
145 150 155 160	
ggc tgt atc ttt agt ctg aaa ttc tgc ggt gct cat gtc gtc act cac	528
Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His	
165 170 175	
ttc ttc tgt gat ggg cca ccc atc ctg tcc ttg tct tgt gta gac acc	576
Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr	
180 185 190	
tca ctg tgt gag atc ctg ctc ttc att ttt gct ggt ttc aac ctt ttg	624
Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu	
195 200 205	
agc tgc acc ctc acc atc ttg atc tcc tac ttc tta att ctc aac acc	672
Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr	
210 215 220	
atc ctg aaa atg agc tcg gcc cag ggc agg ttt aag gca ttt tcc acc	720
Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr	
225 230 235 240	
tgt gca tcc cac ctc act gcc atc tgc ctc ttc ttt ggc aca aca ctt	768
Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu	
245 250 255	
ttt atg tac ctg cgc ccc agg tcc agc tac tcc ttg acc cag gac cgc	816
Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg	
260 265 270	

39/261

aca gtt gct gtc atc tac aca gtg gtg atc cca gtg ctg aac ccc ctc 864  
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu  
           275                          280                          285

atg tac tct ttg aga aac aag gat gtg aag aaa gct tta ata aag ctt 912  
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu  
           290                          295                          300

tta aag aaa ttg ttt ata agc ttt cca gat 942  
 Leu Lys Lys Leu Phe Ile Ser Phe Pro Asp  
           305                          310

<210> 34  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly  
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 Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu  
           20                          25                          30  
 Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu  
           35                          40                          45  
 Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys  
           50                          55                          60  
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln  
           65                          70                          75                          80  
 Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly  
           85                          90                          95  
 Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys  
           100                          105                          110  
 Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn  
           115                          120                          125  
 Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu  
           130                          135                          140  
 Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr  
           145                          150                          155                          160  
 Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His  
           165                          170                          175  
 Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr  
           180                          185                          190  
 Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu  
           195                          200                          205  
 Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr  
           210                          215                          220  
 Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr  
           225                          230                          235                          240  
 Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu  
           245                          250                          255  
 Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg  
           260                          265                          270  
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu  
           275                          280                          285  
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu  
           290                          295                          300  
 Leu Lys Lys Leu Phe Ile Ser Phe Pro Asp  
           305                          310

&lt;210&gt; 35

40/261

<211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)... (942)

<400> 35  
 atg ggt cga gga aac agc act gaa gtg act gaa ttc cat ctt ctg gga 48  
 Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly  
 1 5 10 15

ttt ggt gtc caa cac gaa ttt cag cat gtc ctt ttc att gta ctt ctt 96  
 Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu  
 20 25 30

ctt atc tat gtg acc tcc ctg ata gga aat att gga atg atc tta ctc 144  
 Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu  
 35 40 45

atc aag acc gat tcc aga ctt caa aca ccc atg tac ttt ttt cca caa 192  
 Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln  
 50 55 60

cat ttg gct ttt gtt gat atc tgt tat act tct gct atc act ccc aag 240  
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys  
 65 70 75 80

atg ctc caa agc ttc aca gaa gaa aat aat ttg ata aca ttt cgg ggc 288  
 Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly  
 85 90 95

tgt gtg ata caa ttc tta gtt tat gca aca ttt gca acc agt gac tgt 336  
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys  
 100 105 110

tac ctc cta gct att atg gca atg gat tgt tat gtt gcc atc tgt aag 384  
 Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys  
 115 120 125

ccc ctt cgc tat ccc atg atc atg tcc caa aca gtc tac atc caa ctc 432  
 Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu  
 130 135 140

gta gct ggc tca tat att ata ggc tca ata aat gcc tct gta cat aca 480  
 Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr  
 145 150 155 160

ggt ttt aca tgt tca ctg tcc ttc tgc aag tcc aat agc atc aat cac 528  
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His  
 165 170 175

ttt ttc tgt gat gtt ccc cct att ctt gct ctt tca tgc tcc aat gtt 576  
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val  
 180 185 190

gac atc aac atc atg cta ctt gtt gtc ttt gtg gga tct aac ttg ata 624  
 Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile  
 195 200 205

41/261

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ttc act ggg ttg gtc gtc atc ttt tcc tac atc tac atc atg gcc acc 672
Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
    210                215                220

atc ctg aaa atg tct tct agt gca gga agg aaa aaa tcc ttc tca aca 720
Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
    225                230                235                240

tgt gct tcc cac ctg acc gca gtc acc att ttc tat ggg aca ctc tct 768
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
                245                250                255

tac atg tat ttg cag tct cat tct aat aat tcc cag gaa aat atg aaa 816
Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
                260                265                270

gtg gcc ttt ata ttt tat ggc aca gtt att ccc atg tta aat cct tta 864
Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
    275                280                285

atc tat agc ttg aga aat aag gaa gta aaa gaa gct tta aaa aga cta 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Arg Leu
    290                295                300

cta tgg tct gaa tgt tgt gtc tcc caa aat 942
Leu Trp Ser Glu Cys Cys Val Ser Gln Asn
    305                310

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<210> 36  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 36
Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly
 1          5          10          15
Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
    20          25          30
Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
    35          40          45
Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
    50          55          60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
    65          70          75          80
Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
    85          90          95
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
    100          105          110
Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
    115          120          125
Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
    130          135          140
Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
    145          150          155          160
Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
    165          170          175
Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
    180          185          190
Asp Ile Asn Ile Met Leu Leu Val Phe Val Gly Ser Asn Leu Ile
    195          200          205

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42/261

Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr  
 210 215 220  
 Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser  
 245 250 255  
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys  
 260 265 270  
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Arg Leu  
 290 295 300  
 Leu Trp Ser Glu Cys Cys Val Ser Gln Asn  
 305 310

<210> 37  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(948)

<400> 37  
 atg tta gaa gga aat ctc acc agc gta act gaa ttt gtc atg atg ggc 48  
 Met Leu Glu Gly Asn Leu Thr Ser Val Thr Glu Phe Val Met Met Gly  
 1 5 10 15  
 ttt gct ggc atc cat gaa gca cac ctc ctc ttc ttc ata ctc ttc ctc 96  
 Phe Ala Gly Ile His Glu Ala His Leu Phe Phe Ile Leu Phe Leu  
 20 25 30  
 acc atg tac ctg ttc acc ttg gtg gag aat ttg gcc atc att tta gtg 144  
 Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile Leu Val  
 35 40 45  
 gtg ggt ttg gac cac cga cta cgg aga ccc atg tat ttc ttc ctg aca 192  
 Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 cac ttg tcc tgc ctt gaa atc tgg tac act tct gtt aca gtg ccc aag 240  
 His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val Pro Lys  
 65 70 75 80  
 atg ctg gct ggt ttt att ggg gtg gat ggt ggc aag aat atc tct tat 288  
 Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile Ser Tyr  
 85 90 95  
 gct ggt tgc cta tcc cag ctc ttc atc ttc acc ttt ctt ggg gca act 336  
 Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly Ala Thr  
 100 105 110  
 gag tgt ttc cta ctg gct gcc atg gcc tat gat cgt tat gtg gcc att 384  
 Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile  
 115 120 125  
 tgt atg cct ctc cac tat ggg gct ttt gtg tcc tgg ggc acc tgc atc 432  
 Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr Cys Ile  
 130 135 140



43/261

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cgt ctg gca gct gcc tgt tgg ctg gta ggt ttc ctc aca ccc atc ttg 480
Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro Ile Leu
145                      150                      155                      160

cca atc tac ctc ttg tct cag cta aca ttt tgt ggc cca aat gtc att 528
Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn Val Ile
                      165                      170                      175

gac cat ttc tcc tgt gat gcc tca ccc ttg cta gcc ttg tgc tgc tca 576
Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser Cys Ser
                      180                      185                      190

gat gtc act tgg aag gag act gtg gat ttc ctg gtg tct ctg gct gtg 624
Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu Ala Val
                      195                      200                      205

cta ctg gcc tcc tct atg gtc att gct gtg tcc tat ggc aac atc gtc 672
Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn Ile Val
                      210                      215                      220

tgg aca ctg ctg cac atc cgc tca gct gct gag cgc tgg aag gcc ttc 720
Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys Ala Phe
225                      230                      235                      240

tct acc tgt gca gct cac ctg act gtg gtg agc ctc ttc tat ggc act 768
Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr
                      245                      250                      255

ctt ttc ttt atg tat gtc cag acc aag gtg acc tcc tcc atc aac ttc 816
Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile Asn Phe
                      260                      265                      270

aac aag gtg gta tct gtc ttc tac tct gtt gtc acg ccc atg ctc aat 864
Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met Leu Asn
275                      280                      285

cct ctc atc tac agt ctt agg aac aag gaa gtg aag gga gct ctg ggt 912
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly
290                      295                      300

cga act ctg tct caa aaa aaa aaa aaa aaa aat 948
Arg Thr Leu Ser Gln Lys Lys Lys Lys Lys Lys Asn
305                      310                      315

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<210> 38  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

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<400> 38
Met Leu Glu Gly Asn Leu Thr Ser Val Thr Glu Phe Val Met Met Gly
1      5      10      15
Phe Ala Gly Ile His Glu Ala His Leu Phe Phe Ile Leu Phe Leu
20      25      30
Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile Leu Val
35      40      45
Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe Leu Thr
50      55      60
His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val Pro Lys
65      70      75      80

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44/261

Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile Ser Tyr  
85 90 95  
Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly Ala Thr  
100 105 110  
Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile  
115 120 125  
Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr Cys Ile  
130 135 140  
Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro Ile Leu  
145 150 155 160  
Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn Val Ile  
165 170 175  
Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser Cys Ser  
180 185 190  
Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu Ala Val  
195 200 205  
Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn Ile Val  
210 215 220  
Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys Ala Phe  
225 230 235 240  
Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr  
245 250 255  
Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile Asn Phe  
260 265 270  
Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met Leu Asn  
275 280 285  
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly  
290 295 300  
Arg Thr Leu Ser Gln Lys Lys Lys Lys Lys Lys Asn  
305 310 315

<210> 39  
<211> 942  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(942)

<400> 39  
atg aaa aac aga acc atg ttt ggt gag ttt att cta ctg ggc ctt aca 48  
Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr  
1 5 10 15  
aat caa cct gaa ctc caa gtg atg ata ttc atc ttt ctg ttc ctc acc 96  
Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr  
20 25 30  
tac atg cta agt atc cta gga aat ctg act att atc acc ctc acc tta 144  
Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu  
35 40 45  
cta gac ccc cac ctc cag acc ccc atg tat ttc ttc ctc cgg aat ttc 192  
Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe  
50 55 60  
tcc ttc tta gaa att tcc ttc aca tcc att ttt att ccc aga ttt ctg 240  
Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu  
65 70 75 80

45/261

acc agc atg aca aca gga aat aaa gtt atc agc ttt gct ggc tgc ttg 288  
 Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu  
                     85                    90                    95

act cag tat ttt ttt gct ata ttt ctt gga gct acc gag ttt tac ctc 336  
 Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu  
                     100                    105                    110

ctg gcc tcc atg tct tat gat cgt tat gtg gcc atc tgc aaa ccc ttg 384  
 Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
                     115                    120                    125

cat tac ctg act att atg agc agc aga gtc tgc ata caa cta gtg ttc 432  
 His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe  
                     130                    135                    140

tgc tcc tgg ttg ggg gga ttc cta gca atc tta cca cca atc atc ctg 480  
 Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu  
                     145                    150                    155                    160

atg acc cag gta gat ttc tgt gtc tcc aac att ctg aat cac tat tac 528  
 Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr  
                     165                    170                    175

tgt gac tat ggg cct ctc gtg gag ctt gcc tgc tca gac aca agc ctc 576  
 Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu  
                     180                    185                    190

tta gaa ctg atg atc tcc gtg atg aca gcc acc ata gtc ttc att atg 624  
 Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met  
                     195                    200                    205

atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt gcc 672  
 Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala  
                     210                    215                    220

atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc acc 720  
 Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr  
                     225                    230                    235                    240

tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc agc 768  
 Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser  
                     245                    250                    255

atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac cgc 816  
 Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg  
                     260                    265                    270

gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc atc 864  
 Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile  
                     275                    280                    285

atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac ttg 912  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu  
                     290                    295                    300

ctg cct ttg aga aag tgg ttg aga ata tgg 942  
 Leu Pro Leu Arg Lys Trp Leu Arg Ile Trp  
                     305                    310

&lt;210&gt; 40

46/261

<211> 314  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 40

Met	Lys	Asn	Arg	Thr	Met	Phe	Gly	Glu	Phe	Ile	Leu	Leu	Gly	Leu	Thr
1				5					10					15	
Asn	Gln	Pro	Glu	Leu	Gln	Val	Met	Ile	Phe	Ile	Phe	Leu	Phe	Leu	Thr
		20						25					30		
Tyr	Met	Leu	Ser	Ile	Leu	Gly	Asn	Leu	Thr	Ile	Ile	Thr	Leu	Thr	Leu
	35						40					45			
Leu	Asp	Pro	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg	Asn	Phe
	50					55				60					
Ser	Phe	Leu	Glu	Ile	Ser	Phe	Thr	Ser	Ile	Phe	Ile	Pro	Arg	Phe	Leu
65				70						75					80
Thr	Ser	Met	Thr	Thr	Gly	Asn	Lys	Val	Ile	Ser	Phe	Ala	Gly	Cys	Leu
			85						90					95	
Thr	Gln	Tyr	Phe	Phe	Ala	Ile	Phe	Leu	Gly	Ala	Thr	Glu	Phe	Tyr	Leu
		100						105					110		
Leu	Ala	Ser	Met	Ser	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu
	115						120					125			
His	Tyr	Leu	Thr	Ile	Met	Ser	Ser	Arg	Val	Cys	Ile	Gln	Leu	Val	Phe
	130				135					140					
Cys	Ser	Trp	Leu	Gly	Gly	Phe	Leu	Ala	Ile	Leu	Pro	Pro	Ile	Ile	Leu
145				150						155					160
Met	Thr	Gln	Val	Asp	Phe	Cys	Val	Ser	Asn	Ile	Leu	Asn	His	Tyr	Tyr
			165						170					175	
Cys	Asp	Tyr	Gly	Pro	Leu	Val	Glu	Leu	Ala	Cys	Ser	Asp	Thr	Ser	Leu
	180						185						190		
Leu	Glu	Leu	Met	Ile	Ser	Val	Met	Thr	Ala	Thr	Ile	Val	Phe	Ile	Met
	195						200					205			
Ile	Pro	Phe	Ser	Leu	Ile	Val	Thr	Ser	Tyr	Ile	Arg	Ile	Leu	Gly	Ala
	210					215					220				
Ile	Leu	Ala	Met	Ala	Ser	Thr	Gln	Ser	Arg	Arg	Lys	Val	Phe	Ser	Thr
225				230						235					240
Cys	Ser	Ser	His	Leu	Leu	Val	Val	Ser	Leu	Phe	Phe	Gly	Thr	Ala	Ser
			245						250					255	
Ile	Thr	Tyr	Ile	Arg	Pro	Gln	Ala	Gly	Ser	Ser	Val	Thr	Thr	Asp	Arg
	260							265					270		
Val	Leu	Ser	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu	Asn	Pro	Ile
	275						280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Val	Arg	Arg	Ala	Leu	Arg	His	Leu
	290				295						300				
Leu	Pro	Leu	Arg	Lys	Trp	Leu	Arg	Ile	Trp						
305					310										

<210> 41  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)... (942)

&lt;400&gt; 41

atg	aaa	tca	tgg	aac	aat	aca	ata	att	tta	gaa	ttt	ctt	ctc	ctg	gga
Met	Lys	Ser	Trp	Asn	Asn	Thr	Ile	Ile	Leu	Glu	Phe	Leu	Leu	Leu	Gly
1				5					10					15	

48

47/261

att tca gag gaa cca gaa ttg cag gcc ttc ctc ttt ggg ctg ttc ctg	96
Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu	
20 25 30	
tcc atg tac ctg gtc act gtg ctc ggg aac ctg ctc atc atc ctg gcc	144
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala	
35 40 45	
aca atc tca gac tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc	192
Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
aac ctg tcc ttc gta gac atc tgt ttt gtc tct acc act gtc ccg aag	240
Asn Leu Ser Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys	
65 70 75 80	
atg ctg gtg aac atc cag aca cac aac aaa gtc atc acc tat gca ggc	288
Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly	
85 90 95	
tgc atc acc cag atg tgc ttt ttc tta ctc ttt gta gga ttg gat aac	336
Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn	
100 105 110	
ttc ctt ctg acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac	384
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His	
115 120 125	
cct ctg cac tac atg gtc att atg aac cct caa ctc tgt gga ctg ctg	432
Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu	
130 135 140	
gtt ctg gca tcc tgg atc atg agt gtt ctg aat tcc atg tta caa agc	480
Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser	
145 150 155 160	
tta atg gtg ttg cca ctg ccc ttt tgt aca cac atg gaa atc cct cat	528
Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His	
165 170 175	
ttt ttc tgt gaa att aat cag gtg gtc cac ctt gcc tgt tct gac acc	576
Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr	
180 185 190	
ttt ctt aat gac ata gtg atg tat ttt gca gta gcg ctg ctg ggc ggt	624
Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly	
195 200 205	
ggg ccc ctc act ggg atc ctg tac tct tac tct aag ata gtt tcc tcc	672
Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser	
210 215 220	
ata cgt gca atc tca tca gct cag ggg aag tat aag gca ttt tcc acc	720
Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr	
225 230 235 240	
tgt gca tct cac ctc tca gtt gtc tcc tta ttt tat ggt aca tgc tta	768
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu	
245 250 255	

48/261

ggg gtg tac ctt agt tct gct gcc acc cac aat tca cac aca ggt gct 816  
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala  
 260 265 270  
 gca gcc tca gtg atg tac act gtg gtc acc ccc atg ctg aac ccc ttc 864  
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 atc tac agt ctg agg aat aaa cac ata aag ggt gct atg aaa aca ttc 912  
 Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe  
 290 295 300  
 ttc aga gga aag caa aat aga aag gct att 942  
 Phe Arg Gly Lys Gln Asn Arg Lys Ala Ile  
 305 310

&lt;210&gt; 42

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Met Lys Ser Trp Asn Asn Thr Ile Ile Leu Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly  
 85 90 95  
 Cys Ile Thr Gln Met Cys Phe Leu Leu Phe Val Gly Leu Asp Asn  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu  
 130 135 140  
 Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser  
 145 150 155 160  
 Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly  
 195 200 205  
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser  
 210 215 220  
 Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu  
 245 250 255  
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala  
 260 265 270  
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe  
 290 295 300

49/261

Phe Arg Gly Lys Gln Asn Arg Lys Ala Ile  
305 310

<210> 43  
<211> 936  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)... (936)

<400> 43  
atg ctg aat aca acc tca gtc act gaa ttt ctc ctt ttg gga gtg aca 48  
Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr  
1 5 10 15  
gac att caa gaa ctg cag cct ttt ctc ttc gtt gtt ttc ctt acc atc 96  
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile  
20 25 30  
tac ttc atc agt gtg gct ggg aat gga gcc att ctg atg att gtc atc 144  
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile  
35 40 45  
tct gat cct aga ctc cat tcc cct atg tat ttc ttc ctg gga aac ctg 192  
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu  
50 55 60  
tcc tgc ctg gac atc tgc tac tcc agc gta aca ctg cca aaa atg ctg 240  
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu  
65 70 75 80  
cag aac ttc ctc tct gca cac aaa gca att tct ttc ttg gga tgc ata 288  
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile  
85 90 95  
agc caa ctc cat ttc ttc cac ttc ctg ggc agc aca gag gcc atg ttg 336  
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu  
100 105 110  
ttg gcc gtg atg gca ttt gac cgc ttt gtg gct att tgc aag cca ctt 384  
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu  
115 120 125  
cgc tac act gtc att atg aac cct cag ctc tgt acc cag atg gcc atc 432  
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile  
130 135 140  
aca atc tgg atg att ggt ttt ttc cat gcc ctg ctg cac tcc cta atg 480  
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met  
145 150 155 160  
acc tct cgc ttg aac ttc tgt ggt tct aac cgt atc tat cac ttc ttc 528  
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe  
165 170 175  
tgt gat atc cag cct gtc ctg cag ctg gta tgt gga gac acc tgc ctt 576  
Cys Asp Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser Leu  
180 185 190

50/261

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aat gaa ctg cag att atc ctg gca aca gcc ctc ctc atc ctc tgc ccc 624
Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys Pro
      195                      200                      205

ttt ggc ctc atc ctg ggc tcc tac ggg cgt atc ctc gtt acc atc ttc 672
Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile Phe
      210                      215                      220

cgg atc cca tct gtt gcg ggc cgc cgc aag gcc ttc tcc acc tgc tcc 720
Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
      225                      230                      235                      240

tcc cac ctg atc gtg gtc tcc ctc ttc tat ggc acc gca ctc ttt atc 768
Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe Ile
      245                      250                      255

tat att cgc cct aag gcc agc tac gat cgc gcc act gac cct ctg gtg 816
Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu Val
      260                      265                      270

tcc ctc ttc tat gct gtg gtc acc ccc atc ctc aac ccc atc atc tac 864
Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile Tyr
      275                      280                      285

agc ctg cgg aac aca gag gtc aaa gct gcc cta aag aga acc atc cag 912
Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile Gln
      290                      295                      300

aaa acg gca ttt cac agc agt tgg 936
Lys Thr Ala Phe His Ser Ser Trp
      305                      310

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<210> 44  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

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<400> 44
Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1      5      10      15
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
      20      25      30
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile
      35      40      45
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
      50      55      60
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu
      65      70      75      80
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile
      85      90      95
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu
      100      105      110
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu
      115      120      125
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
      130      135      140
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met
      145      150      155      160
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe
      165      170      175

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51/261

Cys Asp Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser Leu  
 180 185 190  
 Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys Pro  
 195 200 205  
 Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile Phe  
 210 215 220  
 Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe Ile  
 245 250 255  
 Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu Val  
 260 265 270  
 Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile Gln  
 290 295 300  
 Lys Thr Ala Phe His Ser Ser Trp  
 305 310

<210> 45  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (945)

<400> 45  
 atg aat tgg gaa aat gag agc tcc cca aaa gag ttt ata cta ctt ggc 48  
 Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 ttc tca gat agg gct tgg cta caa atg ccc ctt ttt gtg gtc ctg tta 96  
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu  
 20 25 30  
 ata tca tac aca atc acc ata ttt ggc aat gtg tcc atc atg atg gtg 144  
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val  
 35 40 45  
 tgc att ctg gat ccc aaa ctt cat act ccc atg tat ttc ttt ctc act 192  
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 aat ctc tcc atc tta gat ctc tgc tat acc aca act aca gtc cct cat 240  
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His  
 65 70 75 80  
 atg ttg gta aat att ggt tgc aac aaa aag acc atc agc tat gct ggc 288  
 Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly  
 85 90 95  
 tgt gtg gcc cac ctc atc atc ttc ctg gcc cta ggt gct aca gag tgt 336  
 Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys  
 100 105 110  
 ctc ctt ctg gct gtt atg tcc ttt gac aga tat gtg gct gtt tgc aga 384  
 Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg  
 115 120 125

52/261

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ccc ctc cac tat gta gtc atc atg aat tat tgg ttc tgc cta agg atg 432
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
130 135 140

gca gcc ttc tca tgg ctc att ggt ttc ggc aac tca gtg ctg cag tct 480
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
145 150 155 160

tcc ttg act ctt aac atg cca cgc tgt ggt cac cag gaa gtg gac cac 528
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
165 170 175

ttt ttc tgt gag gtg cct gca ctt ctc aag ttg tca tgt gct gac aca 576
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
180 185 190

aag cct att gag gct gag ctc ttc ttc ttt agt gta cta att ctt cta 624
Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
195 200 205

att cca gtg aca ttg atc ctc atc tcc tat ggc ttc ata gct caa gca 672
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
210 215 220

gta tta aaa atc agg tca gca gaa gga cgg caa aaa gca ttt ggg aca 720
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225 230 235 240

tgt ggg tcc cac atg att gtg gtg tcc ctc ttt tat gga aca gcc att 768
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245 250 255

tat atg tat ctt caa cca cct tca tcc acc tct aag gac tgg gga aag 816
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
260 265 270

atg ttc ctc acc ctc ttt tac acc gtc atc act cca agt ctc aac ccg 864
Met Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro
275 280 285

ctc att tac acc tta aga aat aag gac atg aag gat gcc ctg aag aaa 912
Leu Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys
290 295 300

ctg atg aga ttt cac cac aaa tct aca aaa ata 945
Leu Met Arg Phe His His Lys Ser Thr Lys Ile
305 310 315

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<210> 46  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu  
 20 25 30  
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val  
 35 40 45

53 / 261

Cys	Ile	Leu	Asp	Pro	Lys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr
50					55						60				
Asn	Leu	Ser	Ile	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Thr	Thr	Val	Pro	His
65					70					75				80	
Met	Leu	Val	Asn	Ile	Gly	Cys	Asn	Lys	Lys	Thr	Ile	Ser	Tyr	Ala	Gly
				85					90					95	
Cys	Val	Ala	His	Leu	Ile	Ile	Phe	Leu	Ala	Leu	Gly	Ala	Thr	Glu	Cys
			100					105					110		
Leu	Leu	Leu	Ala	Val	Met	Ser	Phe	Asp	Arg	Tyr	Val	Ala	Val	Cys	Arg
			115				120					125			
Pro	Leu	His	Tyr	Val	Val	Ile	Met	Asn	Tyr	Trp	Phe	Cys	Leu	Arg	Met
	130					135					140				
Ala	Ala	Phe	Ser	Trp	Leu	Ile	Gly	Phe	Gly	Asn	Ser	Val	Leu	Gln	Ser
145					150					155				160	
Ser	Leu	Thr	Leu	Asn	Met	Pro	Arg	Cys	Gly	His	Gln	Glu	Val	Asp	His
				165					170					175	
Phe	Phe	Cys	Glu	Val	Pro	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Ala	Asp	Thr
			180					185					190		
Lys	Pro	Ile	Glu	Ala	Glu	Leu	Phe	Phe	Phe	Ser	Val	Leu	Ile	Leu	Leu
			195				200					205			
Ile	Pro	Val	Thr	Leu	Ile	Leu	Ile	Ser	Tyr	Gly	Phe	Ile	Ala	Gln	Ala
	210					215					220				
Val	Leu	Lys	Ile	Arg	Ser	Ala	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
225					230					235				240	
Cys	Gly	Ser	His	Met	Ile	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ala	Ile
				245					250					255	
Tyr	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Ser	Thr	Ser	Lys	Asp	Trp	Gly	Lys
			260					265					270		
Met	Phe	Leu	Thr	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Ser	Leu	Asn	Pro
			275				280					285			
Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Asp	Ala	Leu	Lys	Lys
	290					295					300				
Leu	Met	Arg	Phe	His	His	Lys	Ser	Thr	Lys	Ile					
305					310					315					

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<210> 47
<211> 942
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (942)
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<400> 47																
atg	gag	gga	atg	aac	caa	acc	act	gtt	tca	gac	ttc	ctc	ctt	cta	gga	48
Met	Glu	Gly	Met	Asn	Gln	Thr	Thr	Val	Ser	Asp	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
ctc	tct	gag	tgg	cca	gag	gag	cag	cct	ctt	ctg	ttt	ggc	atc	ttc	ctt	96
Leu	Ser	Glu	Trp	Pro	Glu	Glu	Gln	Pro	Leu	Leu	Phe	Gly	Ile	Phe	Leu	
			20					25					30			
ggc	atg	tac	ctg	gtc	acc	atg	gtg	ggg	aac	ctg	ctc	att	atc	ctg	gcc	144
Gly	Met	Tyr	Leu	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
atc	agc	tct	gac	cca	cac	ctc	cat	act	ccc	atg	tac	ttc	ttt	ctg	gcc	192
Ile	Ser	Ser	Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala	
50						55					60					

54/261

aac	ctg	tca	tta	act	gat	gcc	tgt	ttc	act	tct	gcc	tcc	atc	ccc	aaa	240
Asn	Leu	Ser	Leu	Thr	Asp	Ala	Cys	Phe	Thr	Ser	Ala	Ser	Ile	Pro	Lys	
65					70				75						80	
atg	ctg	gcc	aac	att	cat	acc	cag	agt	cag	atc	atc	tcg	tat	tct	ggg	288
Met	Leu	Ala	Asn	Ile	His	Thr	Gln	Ser	Gln	Ile	Ile	Ser	Tyr	Ser	Gly	
				85				90						95		
tgt	ctt	gca	cag	cta	tat	ttc	ctc	ctt	atg	ttt	ggg	ggc	ctt	gac	aac	336
Cys	Leu	Ala	Gln	Leu	Tyr	Phe	Leu	Leu	Met	Phe	Gly	Gly	Leu	Asp	Asn	
			100				105						110			
tgc	ctg	ctg	gct	gtg	atg	gca	tat	gac	cgc	tat	gtg	gcc	atc	tgc	caa	384
Cys	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Gln	
			115				120					125				
cca	ctc	cat	tac	agc	aca	tct	atg	agt	ccc	cag	ctc	tgt	gca	cta	atg	432
Pro	Leu	His	Tyr	Ser	Thr	Ser	Met	Ser	Pro	Gln	Leu	Cys	Ala	Leu	Met	
			130				135					140				
ctg	ggg	gtg	tgc	tgg	gtg	cta	acc	aac	tgt	cct	gcc	ctg	atg	cac	aca	480
Leu	Gly	Val	Cys	Trp	Val	Leu	Thr	Asn	Cys	Pro	Ala	Leu	Met	His	Thr	
145					150				155						160	
ctg	ttg	ctg	acc	cgc	gtg	gct	ttc	tgt	gcc	cag	aaa	gcc	atc	cct	cat	528
Leu	Leu	Leu	Thr	Arg	Val	Ala	Phe	Cys	Ala	Gln	Lys	Ala	Ile	Pro	His	
				165				170						175		
ttc	tat	tgt	gat	cct	agt	gct	ctc	ctg	aag	ctt	gcc	tgc	tca	gat	acc	576
Phe	Tyr	Cys	Asp	Pro	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Thr	
			180					185					190			
cat	gta	aac	gag	ctg	atg	atc	atc	acc	atg	ggc	ttg	ctg	ttc	ctc	act	624
His	Val	Asn	Glu	Leu	Met	Ile	Ile	Thr	Met	Gly	Leu	Leu	Phe	Leu	Thr	
			195				200					205				
gtt	ccc	ctc	ctg	ctg	atc	gtc	ttc	tcc	tat	gtc	cgc	att	ttc	tgg	gct	672
Val	Pro	Leu	Leu	Leu	Ile	Val	Phe	Ser	Tyr	Val	Arg	Ile	Phe	Trp	Ala	
	210					215					220					
gtg	ttt	gtc	atc	tca	tct	cct	gga	ggg	aga	tgg	aag	gcc	ttc	tct	acc	720
Val	Phe	Val	Ile	Ser	Ser	Pro	Gly	Gly	Arg	Trp	Lys	Ala	Phe	Ser	Thr	
225					230					235					240	
tgt	ggg	tct	cat	ctc	acg	gtg	gtt	ctg	ctc	ttc	tat	ggg	tct	ctt	atg	768
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Leu	Leu	Phe	Tyr	Gly	Ser	Leu	Met	
				245				250						255		
ggg	gtg	tat	tta	ctt	cct	cca	tca	act	tac	tct	aca	gag	agg	gaa	agt	816
Gly	Val	Tyr	Leu	Leu	Pro	Pro	Ser	Thr	Tyr	Ser	Thr	Glu	Arg	Glu	Ser	
			260				265						270			
agg	gct	gct	gtt	ctc	tat	atg	gtg	att	att	ccc	acg	cta	aac	cca	ttc	864
Arg	Ala	Ala	Val	Leu	Tyr	Met	Val	Ile	Ile	Pro	Thr	Leu	Asn	Pro	Phe	
			275				280					285				
att	tat	agc	ttg	agg	aac	aga	gac	atg	aag	gag	gct	ttg	ggg	aaa	ctt	912
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Met	Lys	Glu	Ala	Leu	Gly	Lys	Leu	
			290			295					300					

55/261

ttt cac aga aaa ttt gat agt aaa agg ata  
 Phe His Arg Lys Phe Asp Ser Lys Arg Ile  
 305 310

942

<210> 48  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Met Glu Gly Met Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu  
 20 25 30  
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly  
 85 90 95  
 Cys Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn  
 100 105 110  
 Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln  
 115 120 125  
 Pro Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met  
 130 135 140  
 Leu Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr  
 145 150 155 160  
 Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His  
 165 170 175  
 Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 His Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr  
 195 200 205  
 Val Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala  
 210 215 220  
 Val Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met  
 245 250 255  
 Gly Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser  
 260 265 270  
 Arg Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu  
 290 295 300  
 Phe His Arg Lys Phe Asp Ser Lys Arg Ile  
 305 310

<210> 49  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)... (939)

56/261

<400> 49  
ggc aga gtg aac caa acc act gtt tca gac ttc ctc ctt cta gga ctc 48  
Gly Arg Val Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly Leu  
1 5 10 15

tct gag tgg cca gag gag cag cct ctt ctg ttt ggc atc ttc ctt ggc 96  
Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu Gly  
20 25 30

atg tac ctg gtc acc atg gtg ggg aac ctg ctc att atc ctg gcc atc 144  
Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala Ile  
35 40 45

agc tct gac cca cac ctc cat act ccc atg tac ttc ttt ctg gcc aac 192  
Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn  
50 55 60

ctg tca tta act gat gcc tgt ttc act tct gcc tcc atc ccc aaa atg 240  
Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys Met  
65 70 75 80

ctg gcc aac att cat acc cag agt cag atc atc tgc tat tct ggg tgt 288  
Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly Cys  
85 90 95

ctt gca cag cta tat ttc ctc ctt atg ttt ggt ggc ctt gac aac tgc 336  
Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn Cys  
100 105 110

ctg ctg gct gtg atg gca tat gac cgc tat gtg gcc atc tgc caa cca 384  
Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro  
115 120 125

ctc cat tac agc aca tct atg agt ccc cag ctc tgt gca cta atg ctg 432  
Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met Leu  
130 135 140

ggt gtg tgc tgg gtg cta acc aac tgt cct gcc ctg atg cac aca ctg 480  
Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr Leu  
145 150 155 160

ttg ctg acc cgc gtg gct ttc tgt gcc cag aaa gcc atc cct cat ttc 528  
Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His Phe  
165 170 175

tat tgt gat cct agt gct ctc ctg aag ctt gcc tgc tca gat acc cat 576  
Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr His  
180 185 190

gta aac gag ctg atg atc atc acc atg ggc ttg ctg ttc ctc act gtt 624  
Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr Val  
195 200 205

ccc ctc ctg ctg atc gtc ttc tcc tat gtc cgc att ttc tgg gct gtg 672  
Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala Val  
210 215 220

ttt gtc atc tca tct cct gga ggg aga tgg aag gcc ttc tct acc tgt 720  
Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr Cys  
225 230 235 240

57/261

ggt tct cat ctc acg gtg gtt ctg ctc ttc tat ggg tct ctt atg ggt 768  
 Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met Gly  
 245 250 255

gtg tat tta ctt cct cca tca act tac tct aca gag agg gaa agt agg 816  
 Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser Arg  
 260 265 270

gct gct gtt ctc tat atg gtg att att ccc acg cta aac cca ttc att 864  
 Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe Ile  
 275 280 285

tat agc ttg agg aac aga gac atg aag gag gct ttg ggt aaa ctt ttt 912  
 Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe  
 290 295 300

tgc aga gct ttt agt ttc tca tca tta 939  
 Cys Arg Ala Phe Ser Phe Ser Ser Leu  
 305 310

&lt;210&gt; 50

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

Gly Arg Val Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly Leu  
 1 5 10 15  
 Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu Gly  
 20 25 30  
 Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala Ile  
 35 40 45  
 Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn  
 50 55 60  
 Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys Met  
 65 70 75 80  
 Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly Cys  
 85 90 95  
 Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn Cys  
 100 105 110  
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro  
 115 120 125  
 Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met Leu  
 130 135 140  
 Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr Leu  
 145 150 155 160  
 Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His Phe  
 165 170 175  
 Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr His  
 180 185 190  
 Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr Val  
 195 200 205  
 Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala Val  
 210 215 220  
 Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met Gly  
 245 250 255  
 Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser Arg  
 260 265 270

58/261

Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe Ile  
           275                          280                          285  
 Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe  
           290                          295                          300  
 Cys Arg Ala Phe Ser Phe Ser Ser Leu  
 305                          310

<210> 51  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 51  
 atg aat tgg gta aat gac agc atc ata cag gag ttt att ctg ctg ggt 48  
 Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly  
   1                          5                          10                          15  
  
 ttc tca gat cga cct tgg ctg gag ttt cca ctc ctt gtg gtc ttc ttg 96  
 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu  
                           20                          25                          30  
  
 att tct tac act gtg acc atc ttt ggc aat ctg acc att att cta gtg 144  
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val  
                           35                          40                          45  
  
 tca cgc ctg gac acc aaa ctt cat acc ccc atg tat ttt ttt ctt acc 192  
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
           50                          55                          60  
  
 aat cta tca ctc ctg gat ctt tgt tac acc aca tgt aca gtc cca caa 240  
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Cys Thr Val Pro Gln  
   65                          70                          75                          80  
  
 atg cta gta aat tta tgc agc atc agg aaa gta atc agt tat cgt ggc 288  
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly  
                           85                          90                          95  
  
 tgt gta gcc cag ctt ttc ata ttt ctg gcc ttg ggg gct act gaa tat 336  
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr  
                           100                          105                          110  
  
 ctt ctc ctg gcc gtc atg tcc ttt gat agg ttt gta gct att tgt cgg 384  
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg  
           115                          120                          125  
  
 cct ctc cat tac tca gtt atc atg cac cag aga ctc tgc ctc cag ttg 432  
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu  
   130                          135                          140  
  
 gca gct gca tcc tgg gtt act ggt ttt agt aac tca gtg tgg ttg tct 480  
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser  
   145                          150                          155                          160  
  
 acc ctg act ctc cag ctg cca ctc tgt gac ccc tat gtg ata gat cac 528  
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His  
                           165                          170                          175



59/261

ttt ctc tgt gaa gtc cct gca ctg ctc aag tta tct tgt gtt gag aca 576  
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr  
 180 185 190

aca gca aat gag gct gaa cta ttc ctt gtc agt gag ctc ttc cat cta 624  
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu  
 195 200 205

ata ccc ctg aca ctc atc ctt ata tca tat gct ttt att gtc cga gca 672  
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala  
 210 215 220

gta ttg agg ata cag tct gct gaa ggt cga caa aaa gca ttt ggg aca 720  
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr  
 225 230 235 240

tgt ggt tcc cat cta att gtg gtg tct ctt ttt tat agt aca gcc gtc 768  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val  
 245 250 255

tct gtg tac ctg caa cca cct tcg ccc agc tcc aag gac caa gga aag 816  
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys  
 260 265 270

atg gtt tct ctc ttc tat gga atc att gca ccc atg ctg aat ccc ctt 864  
 Met Val Ser Leu Phe Tyr Gly Ile Ala Pro Met Leu Asn Pro Leu  
 275 280 285

ata tat aca ctt agg aac aag gag gta aag gaa ggc ttt aaa agg ttg 912  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu  
 290 295 300

gtt gca aga cgt tct ttc tgc tca tcc acc 942  
 Val Ala Arg Arg Ser Phe Cys Ser Ser Thr  
 305 310

<210> 52  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu  
 20 25 30  
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val  
 35 40 45  
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly  
 85 90 95  
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr  
 100 105 110  
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu  
 130 135 140

60/261

Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser  
 145 150 155 160  
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His  
 165 170 175  
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr  
 180 185 190  
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu  
 195 200 205  
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala  
 210 215 220  
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val  
 245 250 255  
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys  
 260 265 270  
 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu  
 290 295 300  
 Val Ala Arg Arg Ser Phe Cys Ser Ser Thr  
 305 310

<210> 53  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 53  
 atg gga ttg ggc aat gag agt tcc cta atg gat ttc atc ctt cta ggc 48  
 Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 ttc tca gac cac cct cgt ctg gag gct gtt ctc ttt gta ttt gtc ctt 96  
 Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu  
 20 25 30  
 ttc ttc tac ctc ctg acc ctt gtg gga aac ttc acc ata atc atc atc 144  
 Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile Ile  
 35 40 45  
 tca tat ctg gat ccc cct ctt cat acc cca atg tac ttt ttt ctc agc 192  
 Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 aac ctc tct tta ctg gac atc tgc ttc act act agc ctt gct cct cag 240  
 Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln  
 65 70 75 80  
 acc tta gtt aac ttg caa aga cca aag aag acg atc act tac ggt ggt 288  
 Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly  
 85 90 95  
 tgt gtg gcg caa ctc tat att tct ctg gca ctg ggc tcc act gaa tgt 336  
 Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys  
 100 105 110

61/261

atc ctc ttg gct gac atg gcc ttg gat cgg tac att gct gtc tgc aaa 384  
 Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys  
 115 120 125

ccc ctc cac tat gta gtc atc atg aac cca cgg ctt tgc caa cag ctg 432  
 Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu  
 130 135 140

gca tct atc tcc tgg ctc agt ggt ttg gct agt tcc cta atc cat gca 480  
 Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala  
 145 150 155 160

act ttt acc ttg caa ttg cct ctc tgt ggc aac cat agg ctg gac cat 528  
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His  
 165 170 175

ttt att tgc gaa gta cca gct ctt ctc aag ttg gct tgt gtg gac acc 576  
 Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr  
 180 185 190

act gtc aat gaa ttg gtg ctt ttt gtt gtt agt gtt ctg ttt gtt gtc 624  
 Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val  
 195 200 205

att cca cca gca ctc atc tcc atc tcc tat ggc ttc ata act caa gct 672  
 Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala  
 210 215 220

gtg ctg agg atc aaa tca gta gag gca agg cac aaa gcc ttc agc acc 720  
 Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr  
 225 230 235 240

tgc tcc tcc cac ctt aca gtg gtg att ata ttc tat ggc acc ata atc 768  
 Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile  
 245 250 255

tac gtg tac ctg caa cct agt gac agc tat gcc cag gac caa ggg aag 816  
 Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys  
 260 265 270

ttt atc tcc ctc ttc tac acc atg gtg acc ccc act tta aat cct atc 864  
 Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile  
 275 280 285

atc tat act tta agg aac aag gat atg aaa gag gct ctg agg aaa ctt 912  
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu  
 290 295 300

ctc tgc gga aaa ttg atc tct aaa cag aat 942  
 Leu Ser Gly Lys Leu Ile Ser Lys Gln Asn  
 305 310

&lt;210&gt; 54

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly  
 1 5 10 15

62/261

Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu  
                   20                  25                  30  
 Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile  
                   35                  40                  45  
 Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
                   50                  55                  60  
 Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln  
                   65                  70                  75                  80  
 Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly  
                   85                  90                  95  
 Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys  
                   100                  105                  110  
 Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys  
                   115                  120                  125  
 Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu  
                   130                  135                  140  
 Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala  
                   145                  150                  155                  160  
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His  
                   165                  170                  175  
 Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr  
                   180                  185                  190  
 Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val  
                   195                  200                  205  
 Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala  
                   210                  215                  220  
 Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr  
                   225                  230                  235                  240  
 Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile  
                   245                  250                  255  
 Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys  
                   260                  265                  270  
 Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile  
                   275                  280                  285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu  
                   290                  295                  300  
 Leu Ser Gly Lys Leu Ile Ser Lys Gln Asn  
                   305                  310

&lt;210&gt; 55

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(945)

&lt;400&gt; 55

atg gga aga aat aac cta aca aga ccc tct gaa ttc atc ctc ctt gga 48  
 Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly  
   1                  5                  10                  15  
  
 ctc tcc tct cga cct gag gat cag aag ccg ctc ttt gct gtg ttc ctc 96  
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu  
                   20                  25                  30  
  
 ccc atc tac ctt atc aca gtg ata gga aac ctg ctt atc atc ctg gcc 144  
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala  
                   35                  40                  45

63/261

atc cgc tca gac act cgt ctc cag acg ccc atg tac ttc ttt cta agc	192
Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
atc ctg tct ttt gtt gac att tgc tat gtg aca gtc att atc cct aag	240
Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys	
65 70 75 80	
atg ctg gtg aac ttc tta tca gag aca aag acc atc tct tac ggt gag	288
Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu	
85 90 95	
tgt ctg acc cag atg tac ttt ttc tta gcc ttt gga aac aca gac agt	336
Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser	
100 105 110	
tac ctg cta gca gcc atg gcc att gac cgc tat gtg gcc ata tgt aat	384
Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn	
115 120 125	
ccc ttc cac tac atc acc att atg agt cac aga tgc tgt gtc ctg ctt	432
Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu	
130 135 140	
ctg gtt ctc tcc ttc tgc att cca cat ttt cac tcc ctc ctg cac att	480
Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile	
145 150 155 160	
ctt ctg act aat cag ctc atc ttc tgt gcc tcc aat gtc atc cat cac	528
Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His	
165 170 175	
ttt ttc tgc gat gat caa cca cct gtg cta aag ctc tcc tgc tct gac	576
Phe Phe Cys Asp Asp Gln Pro Pro Val Leu Lys Leu Ser Cys Ser Asp	
180 185 190	
aca tcc tcc agc cag atg gtg gtg atg act gag acc tta gct gtc att	624
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile	
195 200 205	
gtg acc ccc ttc ctg tgt acc atc ttc tcc tac ctg caa atc atc gtc	672
Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val	
210 215 220	
act gtg ctc aga atc ccc tct gca gcc ggg aag tgg aag gcc ttc tct	720
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser	
225 230 235 240	
acc tgt ggc tcc cac ctc act gta gtg gtc ctg ttc tat ggg agt gtc	768
Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val	
245 250 255	
atc tat gtc tat ttt agg cct ctg tcc atg tac tca gtg atg aag ggc	816
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly	
260 265 270	
cgg gta gcc aca gtt atg tac aca gta gtg aca ccc atg ctg aac cct	864
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro	
275 280 285	

64/261

ttc atc tac agc ctg agg aac aaa gat atg aaa agg ggt ttg aag aaa 912  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys  
 290 295 300

tta aga cac aga gaa ttt act cat aga aag aac 945  
 Leu Arg His Arg Glu Phe Thr His Arg Lys Asn  
 305 310 315

<210> 56  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu  
 20 25 30  
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser  
 100 105 110  
 Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu  
 130 135 140  
 Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile  
 145 150 155 160  
 Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His  
 165 170 175  
 Phe Phe Cys Asp Asp Gln Pro Pro Val Leu Lys Leu Ser Cys Ser Asp  
 180 185 190  
 Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile  
 195 200 205  
 Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val  
 210 215 220  
 Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val  
 245 250 255  
 Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly  
 260 265 270  
 Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys  
 290 295 300  
 Leu Arg His Arg Glu Phe Thr His Arg Lys Asn  
 305 310 315

<210> 57  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

65/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(942)

&lt;400&gt; 57

atg acc atg gaa aat tat tct atg gca gct cag ttt gtc tta gat ggt	48
Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly	
1 5 10 15	
tta aca cag caa gca gag ctc cag ctg ccc ctc ttc ctc ctg ttc ctg	96
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu	
20 25 30	
gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc atg att ctc ctg	144
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu	
35 40 45	
att gca gtc agc cct cta ctt cac acc ccc atg tac tat ttc ctc agc	192
Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser	
50 55 60	
agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc att act ccc aaa	240
Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys	
65 70 75 80	
atg ctg gtg aac ttc cta gga aag aag aat aca atc ctt tac tct gag	288
Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu	
85 90 95	
tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg gtg gct gag ggt	336
Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly	
100 105 110	
tac ctc ctg act gcc atg gca tat gat cgc tat gtt gcc atc tgt agc	384
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser	
115 120 125	
cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc tgc tca ctg cta	432
Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu	
130 135 140	
gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc ttg act cat aca	480
Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr	
145 150 155 160	
agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac att atc aac cat	528
Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His	
165 170 175	
tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc tgc tcc aac aca	576
Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr	
180 185 190	
cac ctc aat gag ctt cta ctt ttt atc att gcg ggg ttt aac acc ttg	624
His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu	
195 200 205	
gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc atc ctc tac agc	672
Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser	
210 215 220	

66/261

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atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa gct ttt gga aca 720
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225                230                235                240

tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt ggg tcc att acc 768
Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
                245                250                255

ttc atg tat ttc aag ccc cct tca agt aac tcc ctg gac cag gag aag 816
Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
                260                265                270

gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg ctg aac cct tta 864
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
                275                280                285

ata tac agt ctg agg aat aag gat gtg aag aaa gca tta agg aag gtc 912
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val
                290                295                300

tta agg agg agg aga cag cct agc aga tgg 942
Leu Arg Arg Arg Arg Gln Pro Ser Arg Trp
305                310

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<210> 58  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 58
Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
1          5          10          15
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20          25          30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
35          40          45
Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50          55          60
Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
65          70          75          80
Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
85          90          95
Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
100         105         110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
115         120         125
Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
130         135         140
Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
145         150         155         160
Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
165         170         175
Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
180         185         190
His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
195         200         205
Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
210         215         220
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225         230         235         240

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[illegible]

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<220>
<221> CDS
<222> (1) ... (939)
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<400>	59																	
cga ggc aga aat caa acg gaa gta aca gaa ttt ctc ctc tta gga ctt																		48
Arg Gly Arg Asn Gln Thr Glu Val Thr Glu Phe Leu Leu Leu Gly Leu																		
1				5					10					15				
tcc gac aat cca gat cta caa gga gtc ctc ttt gca ttg ttt ctg ttg																		96
Ser Asp Asn Pro Asp Leu Gln Gly Val Leu Phe Ala Leu Phe Leu Leu																		
			20					25						30				
atc tat atg gca aac atg gtg ggc aat ttg ggg atg att gta ttg att																		144
Ile Tyr Met Ala Asn Met Val Gly Asn Leu Gly Met Ile Val Leu Ile																		
		35					40						45					
aag att gat ctc tgt ctc cac acc ccc atg tat ttc ttt ctc agt agc																		192
Lys Ile Asp Leu Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Ser																		
	50					55						60						
ctc tct ttt gta gat gcc tct tac tct tct tcc gtc act ccc aag atg																		240
Leu Ser Phe Val Asp Ala Ser Tyr Ser Ser Ser Val Thr Pro Lys Met																		
65					70					75							80	
ctg gtg aac ctc atg gct gag aat aag gcc att tct ttt cat gga tgt																		288
Leu Val Asn Leu Met Ala Glu Asn Lys Ala Ile Ser Phe His Gly Cys																		
				85				90						95				
gct gcc cag ttc tac ttc ttt ggc tcc ttc ctg ggg act gag tgc ttc																		336
Ala Ala Gln Phe Tyr Phe Phe Gly Ser Phe Leu Gly Thr Glu Cys Phe																		
			100					105						110				
ctg ttg gcc atg atg gca tat gac cgc tat gca gcc att tgg aac ccc																		384
Leu Leu Ala Met Met Ala Tyr Asp Arg Tyr Ala Ala Ile Trp Asn Pro																		
		115					120						125					
ctg ctc tac cca gtt ctc gtg tct ggg aga att tgc ttt ttg cta ata																		432
Leu Leu Tyr Pro Val Leu Val Ser Gly Arg Ile Cys Phe Leu Leu Ile																		
	130					135					140							
gct acc tcc ttc tta gca ggt tgt gga aat gca gcc ata cat aca ggg																		480
Ala Thr Ser Phe Leu Ala Gly Cys Gly Asn Ala Ala Ile His Thr Gly																		
145					150				155								160	

68/261

atg act ttt agg ttg tcc ttt tgt ggt tct aat agg atc aac cat ttc 528  
Met Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Arg Ile Asn His Phe  
165 170 175

tac tgt gac acc ccg cca ctg ctc aaa ctc tct tgc tct gat acc cac 576  
Tyr Cys Asp Thr Pro Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His  
180 185 190

ttc aat ggc att gtg atc atg gca ttc tca agt ttt att gtc atc agc 624  
Phe Asn Gly Ile Val Ile Met Ala Phe Ser Ser Phe Ile Val Ile Ser  
195 200 205

tgt gtt atg att gtc ctc att tcc tac ctg tgt atc ttc att gcc gtc 672  
Cys Val Met Ile Val Leu Ile Ser Tyr Leu Cys Ile Phe Ile Ala Val  
210 215 220

ttg aag atg cct tcg tta gag ggc agg cac aaa gcc ttc tcc acc tgt 720  
Leu Lys Met Pro Ser Leu Glu Gly Arg His Lys Ala Phe Ser Thr Cys  
225 230 235 240

gcc tct tac ctc atg gct gtc acc ata ttc ttt gga aca atc ctc ttc 768  
Ala Ser Tyr Leu Met Ala Val Thr Ile Phe Phe Gly Thr Ile Leu Phe  
245 250 255

atg tac ttg cgc cct aca tct agc tac tca atg gag caa gac aag gtt 816  
Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Met Glu Gln Asp Lys Val  
260 265 270

gtc tct gtc ttt tat aca gta ata atc cct gtg cta aat ccc ctc atc 864  
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Val Leu Asn Pro Leu Ile  
275 280 285

tat agt tta aaa aat aag gat gta aaa aag gcc cta aag aag atc tta 912  
Tyr Ser Leu Lys Asn Lys Asp Val Lys Lys Ala Leu Lys Lys Ile Leu  
290 295 300

tgg aaa cac atc ttg cac agc cca aat 939  
Trp Lys His Ile Leu His Ser Pro Asn  
305 310

&lt;210&gt; 60

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

Arg Gly Arg Asn Gln Thr Glu Val Thr Glu Phe Leu Leu Leu Gly Leu  
1 5 10 15  
Ser Asp Asn Pro Asp Leu Gln Gly Val Leu Phe Ala Leu Phe Leu Leu  
20 25 30  
Ile Tyr Met Ala Asn Met Val Gly Asn Leu Gly Met Ile Val Leu Ile  
35 40 45  
Lys Ile Asp Leu Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Ser  
50 55 60  
Leu Ser Phe Val Asp Ala Ser Tyr Ser Ser Ser Val Thr Pro Lys Met  
65 70 75 80  
Leu Val Asn Leu Met Ala Glu Asn Lys Ala Ile Ser Phe His Gly Cys  
85 90 95  
Ala Ala Gln Phe Tyr Phe Phe Gly Ser Phe Leu Gly Thr Glu Cys Phe  
100 105 110

69/261

Leu Leu Ala Met Met Ala Tyr Asp Arg Tyr Ala Ala Ile Trp Asn Pro  
           115                  120                  125  
 Leu Leu Tyr Pro Val Leu Val Ser Gly Arg Ile Cys Phe Leu Leu Ile  
       130                  135                  140  
 Ala Thr Ser Phe Leu Ala Gly Cys Gly Asn Ala Ala Ile His Thr Gly  
   145                  150                  155                  160  
 Met Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Arg Ile Asn His Phe  
           165                  170                  175  
 Tyr Cys Asp Thr Pro Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His  
           180                  185                  190  
 Phe Asn Gly Ile Val Ile Met Ala Phe Ser Ser Phe Ile Val Ile Ser  
           195                  200                  205  
 Cys Val Met Ile Val Leu Ile Ser Tyr Leu Cys Ile Phe Ile Ala Val  
   210                  215                  220  
 Leu Lys Met Pro Ser Leu Glu Gly Arg His Lys Ala Phe Ser Thr Cys  
   225                  230                  235                  240  
 Ala Ser Tyr Leu Met Ala Val Thr Ile Phe Phe Gly Thr Ile Leu Phe  
           245                  250                  255  
 Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Met Glu Gln Asp Lys Val  
           260                  265                  270  
 Val Ser Val Phe Tyr Thr Val Ile Ile Pro Val Leu Asn Pro Leu Ile  
           275                  280                  285  
 Tyr Ser Leu Lys Asn Lys Asp Val Lys Lys Ala Leu Lys Lys Ile Leu  
   290                  295                  300  
 Trp Lys His Ile Leu His Ser Pro Asn  
   305                  310

<210> 61  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 61  
 atg gag ata aag aac tac agc agc agc acc tca ggc ttc atc ctc ctg 48  
 Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu  
   1                  5                  10                  15  
  
 ggc ctc tct tcc aac cct cag ctg cag aaa cct ctc ttt gcc atc ttc 96  
 Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe  
           20                  25                  30  
  
 ctc atc atg tac ctg ctc gct gcg gtg ggg aat gtg ctc atc atc ccg 144  
 Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro  
           35                  40                  45  
  
 gcc atc tac tct gac ccc agg ctc cac acc cct atg tac ttt ttt ctc 192  
 Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
   50                  55                  60  
  
 agc aac ttg tct ttc atg gat atc tgc ttc aca aca gtc ata gtg cct 240  
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro  
   65                  70                  75                  80  
  
 aag atg ctg gtg aat ttt cta tca gag aca aag gtt atc tcc tat gtg 288  
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val  
           85                  90                  95

70/261

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ggc tgc ctg gcc cag atg tac ttc ttt atg gca ttt ggg aac act gac 336
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
      100                      105                      110

agc tac ctg ctg gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc 384
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
      115                      120                      125

aac ccc tta cac tat gat gtg gtt atg aaa cca cgg cat tgc ctg ctc 432
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
      130                      135                      140

atg cta ttg ggt tct tgc agc atc tcc cac cta cat tcc ctg ttc cgc 480
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
      145                      150                      155                      160

gtg cta ctt atg tct cgc ttg tct ttc tgt gcc tct cac atc att aag 528
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
      165                      170                      175

cac ttt ttc tgt gac acc cag cct gtg cta aag ctc tcc tgc tct gac 576
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
      180                      185                      190

aca tcc tcc agc cag atg gtg gtg atg act gag acc tta gct gtc att 624
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195                      200                      205

gtg acc ccc ttc ctg tgt atc atc ttc tcc tac ctg cga atc atg gtc 672
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
      210                      215                      220

act gtg ctc aga atc ccc tct gca gcc ggg aag tgg aag gcc ttc tct 720
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
      225                      230                      235                      240

acc tgt ggc tcc cac ctc act gca gta gcc ctt ttc tat ggg agt att 768
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
      245                      250                      255

att tat gtc tat ttt agg ccc ctg tcc atg tac tca gtg gtt agg gac 816
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
      260                      265                      270

cgg gta gcc aca gtt atg tac aca gta gtg aca ccc atg ctg aac cct 864
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275                      280                      285

ttc atc tac agc ctg agg aac aaa gat atg aag agg gag atc aag aag 912
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Glu Ile Lys Lys
      290                      295                      300

aaa ctc tca aaa cga aca aag gaa cac tcc ccc 945
Lys Leu Ser Lys Arg Thr Lys Glu His Ser Pro
      305                      310                      315

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&lt;210&gt; 62

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

71/261

&lt;400&gt; 62

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Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1           5           10           15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
          20           25           30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
          35           40           45
Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
          65           70           75           80
Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
          85           90           95
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
          100           105           110
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
          115           120           125
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
          130           135           140
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
          145           150           155           160
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
          165           170           175
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
          180           185           190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
          195           200           205
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
          210           215           220
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
          225           230           235           240
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
          245           250           255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
          260           265           270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
          275           280           285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Glu Ile Lys Lys
          290           295           300
Lys Leu Ser Lys Arg Thr Lys Glu His Ser Pro
          305           310           315

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&lt;210&gt; 63

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(939)

&lt;400&gt; 63

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atg aag aga aag aac ttc aca gaa gtg tca gaa ttc att ttc ttg gga 48
Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1           5           10           15

ttt tct agc ttt gga aag cat cag ata acc ctc ttt gtg gtt ttc cta 96
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
          20           25           30

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72/261

act gtc tac att tta act ctg gtt gct aac atc atc att gtg act atc	144
Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile	
35 40 45	
atc tgc att gac cat cat ctc cac act ccc atg tat ttc ttc cta agc	192
Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
atg ctg gct agt tca gag acg gtg tac aca ctg gtc att gtg cca cga	240
Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg	
65 70 75 80	
atg ctt ttg agc ctc att ttt cat aac caa cct atc tcc ttg gca ggc	288
Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly	
85 90 95	
tgt gct aca caa atg ttc ttt ttt gtt atc ttg gcc act aat aat tgc	336
Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys	
100 105 110	
ttc ctg ctt act gca atg ggg tat gac cgc tat gtg gcc atc tgc aga	384
Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg	
115 120 125	
ccc ctg aga tac act gtc atc atg agc aag gga cta tgt gcc cag ctg	432
Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu	
130 135 140	
gtg tgt ggg tcc ttt ggc att ggt ctg act atg gca gtt ctc cat gtg	480
Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val	
145 150 155 160	
aca gcc atg ttc aat ttg ccg ttc tgt ggc aca gtg gta gac cac ttc	528
Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe	
165 170 175	
ttt tgt gac att tac cca gtc atg aaa ctt tct tgc att gat acc act	576
Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr	
180 185 190	
atc aat gag ata ata aat tat ggt gta agt tca ttt gtg att ttt gtg	624
Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val	
195 200 205	
ccc ata ggc ctg ata ttt atc tcc tat gtc ctt gtc atc tct tcc atc	672
Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile	
210 215 220	
ctt caa att gcc tca gct gag ggc cgg aag aag acc ttt gcc acc tgt	720
Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys	
225 230 235 240	
gtc tcc cac ctc act gtg gtt att gtc cac tgt ggc tgt gcc tcc att	768
Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile	
245 250 255	
gcc tac ctc aag ccg aag tca gaa agt tca ata gaa aaa gac ctt gtt	816
Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val	
260 265 270	

73/261

ctc tca gtg acg tac acc atc atc act ccc ttg ctg aac cct gtt gtt 864  
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
           275                                  280                                  285

tac agt ctg aga aac aag gag gta aag gat gcc cta tgc aga gta ctt 912  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu  
           290                                  295                                  300

tct aag aga cac agg tat gga aac atc 939  
 Ser Lys Arg His Arg Tyr Gly Asn Ile  
           305                                  310

<210> 64  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly  
   1                                  5                                  10                                  15  
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu  
           20                                  25                                  30  
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile  
           35                                  40                                  45  
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
           50                                  55                                  60  
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg  
   65                                  70                                  75                                  80  
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly  
           85                                  90                                  95  
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys  
           100                                  105                                  110  
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
           115                                  120                                  125  
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu  
           130                                  135                                  140  
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val  
   145                                  150                                  155                                  160  
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe  
           165                                  170                                  175  
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr  
           180                                  185                                  190  
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val  
           195                                  200                                  205  
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile  
           210                                  215                                  220  
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys  
   225                                  230                                  235                                  240  
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile  
           245                                  250                                  255  
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val  
           260                                  265                                  270  
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
           275                                  280                                  285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu  
           290                                  295                                  300  
 Ser Lys Arg His Arg Tyr Gly Asn Ile  
           305                                  310

&lt;210&gt; 65

74/261

<211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

&lt;400&gt; 65

atg gct gca gga aat cac tct aca gtg aca gag ttc att ctc aag ggt	48
Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly	
1 5 10 15	
tta acg aag aga gca gac ctc cag ctc ccc ctc ttt ctc ctc ttc ctc	96
Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu	
20 25 30	
ggg atc tac ttg gtc acc atc gtg ggg aac ctg ggc atg atc act cta	144
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu	
35 40 45	
att tgt ctg aac tct cag ctg cac acc ccc atg tac tac ttt ctc agc	192
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser	
50 55 60	
aat ctg tca ctc atg gat ctc tgc tac tcc tcc gtc att acc cct aag	240
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys	
65 70 75 80	
atg ctg gtg aac ttt gtg tca gag aaa aac atc atc tcc tac gca ggg	288
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly	
85 90 95	
tgc atg tca cag ctc tac ttc ttc ctt gtt ttt gtc att gct gag tgt	336
Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys	
100 105 110	
tac atg ctg aca gtg atg gcc tac gac cgc tat gtt gcc atc tgc cac	384
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His	
115 120 125	
cct ttg ctt tac aac atc att atg tct cat cac acc tgc ctg ctg ctg	432
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu	
130 135 140	
gtg gct gtg gtc tac gcc atc gga ctc att ggc tcc aca ata gaa act	480
Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr	
145 150 155 160	
ggc ctc atg tta aaa ctg ccc tat tgt gag cac ctc atc agt cac tac	528
Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr	
165 170 175	
ttc tgt gac atc ctc cct ctc atg aag ctg tcc tgc tct agc acc tat	576
Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr	
180 185 190	
gat gtt gag atg aca gtc ttc ttt tgc gct gga ttc aac atc ata gtc	624
Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val	
195 200 205	



75/261

acg agc tta aca gtt ctt gtt tct tac acc ttc att ctc tcc agc atc 672  
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile  
 210 215 220

ctc ggc atc agc acc aca gag ggg aga tcc aaa gcc ttc agc acc tgc 720  
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys  
 225 230 235 240

agc tcc cac ctt gca gcc gtg gga atg ttc tat gga tca act gca ttc 768  
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe  
 245 250 255

atg tac tta aaa ccc tcc aca atc agt tcc ttg acc cag gag aat gtg 816  
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val  
 260 265 270

gcc tct gtg ttc tac acc acg gta atc ccc atg ttg aat ccc cta atc 864  
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285

tac agc ctg agg aac aag gaa gta aag gct gcc gtg cag aaa acg ctg 912  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu  
 290 295 300

agg ggt aaa ctg agc ccg cat tcc tgg 939  
 Arg Gly Lys Leu Ser Pro His Ser Trp  
 305 310

&lt;210&gt; 66

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly  
 1 5 10 15  
 Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu  
 35 40 45  
 Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys  
 100 105 110  
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu  
 130 135 140  
 Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr  
 145 150 155 160  
 Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr  
 165 170 175  
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190  
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val  
 195 200 205

76/261

Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile  
 210 215 220  
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe  
 245 250 255  
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val  
 260 265 270  
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu  
 290 295 300  
 Arg Gly Lys Leu Ser Pro His Ser Trp  
 305 310

<210> 67  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 67  
 atg gag aat aat aca gag gtg agt gaa ttc atc ctg ctt ggt cta acc 48  
 Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 aat gcc cca gaa cta cag gtt ccc ctc ttt atc atg ttt acc ctc atc 96  
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile  
 20 25 30  
 tac ctc atc act ctg act ggg aac ctg ggg atg atc ata tta atc ctg 144  
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu  
 35 40 45  
 ctg gac tct cat ctc cac act ccc atg tac ttt ttt ctc agt aac ctg 192  
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 tct ctt gca ggc att ggt tac tcc tca gct gtc act cca aag gtt tta 240  
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu  
 65 70 75 80  
 act ggg ttg ctt ata gaa gac aaa gcc atc tcc tac agt gcc tgt gct 288  
 Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala  
 85 90 95  
 gct cag atg ttc ttt tgt gca gtc ttt gcc act gtg gaa aat tac ctc 336  
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu  
 100 105 110  
 ttg tcc tca atg gcc tat gac cgc tac gca gca gtg tgt aac ccc cta 384  
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu  
 115 120 125  
 cat tat acc acc acc atg aca aca cgt gtg tgt gct tgt ctg gct ata 432  
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile  
 130 135 140

77/261

ggc ttc act ggc tcc tac atc tgt gga ctc ttt caa tcc tcc atc cat 480  
 Gly Phe Thr Gly Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His  
 145 150 155 160  
 gtt gct ttt act ttc cat ctc tcc ttc tgt cat tct aat gtg gtt aat 528  
 Val Ala Phe Thr Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn  
 165 170 175  
 cac ttt ttt tgt gat att cca cca ctc tta gct ctt tct tgc tct gat 576  
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp  
 180 185 190  
 att tac gca cat gag att gtg ctc ttc ata ttg gca gca ttt aat atc 624  
 Ile Tyr Ala His Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile  
 195 200 205  
 ttt ttc act ctc ttg att atc ttg aac tct tat gtt ttt att ttt att 672  
 Phe Phe Thr Leu Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile  
 210 215 220  
 gct atc ctg agg atg cat tca gct gag gga caa aag aag gtc ttt tcc 720  
 Ala Ile Leu Arg Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser  
 225 230 235 240  
 acc tgt gcc tat cac ctc act act gtt tcc atc ttc tat ggg aca atc 768  
 Thr Cys Ala Tyr His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile  
 245 250 255  
 acc ttt atg tac tta cag cca agt tct ggt cat tcc atg gac aca gac 816  
 Thr Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp  
 260 265 270  
 aaa atc tca tct gtg ttc tac acc atg gtc atc ccc atg ctt aac cct 864  
 Lys Ile Ser Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 cta gtc tat agc ctg agg aac aaa gaa gtc cag agt gca ttc aag gtg 912  
 Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val  
 290 295 300  
 gtt att gga aaa gca aag tct tca ttg ggc tta 945  
 Val Ile Gly Lys Ala Lys Ser Ser Leu Gly Leu  
 305 310 315

&lt;210&gt; 68

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile  
 20 25 30  
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu  
 35 40 45  
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu  
 65 70 75 80

78/261

Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala  
 85 90 95  
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu  
 100 105 110  
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu  
 115 120 125  
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile  
 130 135 140  
 Gly Phe Thr Gly Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His  
 145 150 155 160  
 Val Ala Phe Thr Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn  
 165 170 175  
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp  
 180 185 190  
 Ile Tyr Ala His Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile  
 195 200 205  
 Phe Phe Thr Leu Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile  
 210 215 220  
 Ala Ile Leu Arg Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Ala Tyr His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile  
 245 250 255  
 Thr Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp  
 260 265 270  
 Lys Ile Ser Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val  
 290 295 300  
 Val Ile Gly Lys Ala Lys Ser Ser Leu Gly Leu  
 305 310 315

<210> 69  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 69  
 atg gaa tcc tgg aac agc tca tca gtg acc atg ttc atc ctc ctg gga 48  
 Met Glu Ser Trp Asn Ser Ser Ser Val Thr Met Phe Ile Leu Leu Gly  
 1 5 10 15  
 ttc aca gac cat cca gaa ctc cag gcc ctc ctc ttt gtg acc ttc ctg 96  
 Phe Thr Asp His Pro Glu Leu Gln Ala Leu Leu Phe Val Thr Phe Leu  
 20 25 30  
 ggc atc tat ctt acc acc ctg gcc tgg aac ctg gcc ctc att ttt ctg 144  
 Gly Ile Tyr Leu Thr Thr Leu Ala Trp Asn Leu Ala Leu Ile Phe Leu  
 35 40 45  
 atc aga ggt gac acc cat ctg cac aca ccc atg tac ttc ttc cta agc 192  
 Ile Arg Gly Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 aac tta tct ttc att gac atc tgc tac tct tct gct gtg gct ccc aat 240  
 Asn Leu Ser Phe Ile Asp Ile Cys Tyr Ser Ser Ala Val Ala Pro Asn  
 65 70 75 80

79/261

atg ctc act gac ttc ttc tgg gag cag aag acc ata tca ttt gtg ggc	288
Met Leu Thr Asp Phe Phe Trp Glu Gln Lys Thr Ile Ser Phe Val Gly	
85 90 95	
tgt gct gct cag ttt ttt ttc ttt gtc ggc atg ggt ctg tct gag tgc	336
Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu Ser Glu Cys	
100 105 110	
ctc ctc ctg act gct atg gca tac gac cga tat gca gcc atc tcc agc	384
Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Ser Ser	
115 120 125	
ccc ctt ctc tac ccc act atc atg acc cag ggc ctc tgt aca cgc atg	432
Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys Thr Arg Met	
130 135 140	
gtg gtt ggg gca tat gtt ggt ggc ttc ctg agc tcc ctg atc cag gcc	480
Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu Ile Gln Ala	
145 150 155 160	
agc tcc ata ttt agg ctt cac ttt tgc gga ccc aac atc atc aac cac	528
Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile Ile Asn His	
165 170 175	
ttc ttc tgc gac ctc cca cca gtc ctg gct ctg tct tgc tct gac acc	576
Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp Thr	
180 185 190	
ttc ctc agt caa gtg gtg aat ttc ctc gtg gtg gtc act gtc gga gga	624
Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr Val Gly Gly	
195 200 205	
aca tgc ttc ctc caa ctc ctt atc tcc tat ggt tac ata gtg tct gcg	672
Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile Val Ser Ala	
210 215 220	
gtc ctg aag atc cct tca gca gag ggc cga tgg aaa gcc tgc aac acg	720
Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala Cys Asn Thr	
225 230 235 240	
tgt gcc tgc cat ctg atg gtg gtg act ctg ctg ttt ggg aca gcc ctt	768
Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly Thr Ala Leu	
245 250 255	
ttc gtg tac ttg cga ccc agc tcc agc tac ttg cta ggc agg gac aag	816
Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly Arg Asp Lys	
260 265 270	
gtg gtg tct gtt ttc tat tca ttg gtg atc ccc atg ctg aac cct ctc	864
Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro Leu	
275 280 285	
att tac agt ttg agg aac aaa gag atc aag gat gcc ctg tgg aag gtg	912
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Trp Lys Val	
290 295 300	
ttg gaa agg aag aaa att cct tca ccc tgg	942
Leu Glu Arg Lys Lys Ile Pro Ser Pro Trp	
305 310	

&lt;210&gt; 70

80/261

<211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 70

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Met Glu Ser Trp Asn Ser Ser Ser Val Thr Met Phe Ile Leu Leu Gly
 1           5           10           15
Phe Thr Asp His Pro Glu Leu Gln Ala Leu Leu Phe Val Thr Phe Leu
 20           25           30
Gly Ile Tyr Leu Thr Thr Leu Ala Trp Asn Leu Ala Leu Ile Phe Leu
 35           40           45
Ile Arg Gly Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ile Asp Ile Cys Tyr Ser Ser Ala Val Ala Pro Asn
 65           70           75           80
Met Leu Thr Asp Phe Phe Trp Glu Gln Lys Thr Ile Ser Phe Val Gly
 85           90           95
Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu Ser Glu Cys
 100          105          110
Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Ser Ser
 115          120          125
Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys Thr Arg Met
 130          135          140
Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu Ile Gln Ala
 145          150          155          160
Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile Ile Asn His
 165          170          175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp Thr
 180          185          190
Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr Val Gly Gly
 195          200          205
Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile Val Ser Ala
 210          215          220
Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala Cys Asn Thr
 225          230          235          240
Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly Thr Ala Leu
 245          250          255
Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly Arg Asp Lys
 260          265          270
Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Trp Lys Val
 290          295          300
Leu Glu Arg Lys Lys Ile Pro Ser Pro Trp
305          310

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<210> 71  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(942)

<400> 71

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atg gat gga acc aat ggc agc acc caa acc cat ttc atc cta ctg gga
Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
 1           5           10           15

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48

81/261

ttc tct gac cga ccc cat ctg gag agg atc ctc ttt gtg gtc atc ctg	96
Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu	
20 25 30	
atc gcg tac ctc ctg acc ctc gta ggc aac acc acc atc atc ctg gtg	144
Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val	
35 40 45	
tcc cgg ctg gac ccc cac ctc cac acc ccc atg tac ttc ttc ctc gcc	192
Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala	
50 55 60	
cac ctt tcc ttc ctg gac ctc agt ttc acc acc agc tcc atc ccc cag	240
His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln	
65 70 75 80	
ctg ctc tac aac ctt aat gga tgt gac aag acc atc agc tac atg ggc	288
Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly	
85 90 95	
tgt gcc atc cag ctc ttc ctg ttc ctg ggt ctg ggt ggt gtg gag tgc	336
Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys	
100 105 110	
ctg ctt ctg gct gtc atg gcc tat gac cgg tgt gtg gct atc tgc aag	384
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys	
115 120 125	
ccc ctg cac tac atg gtg atc atg aac ccc agg ctc tgc cgg ggc ttg	432
Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu	
130 135 140	
gtg tca gtg acc tgg ggc tgt ggg gtg gcc aac tcc ttg gcc atg tct	480
Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser	
145 150 155 160	
cct gtg acc ctg cgc tta ccc cgc tgt ggg cac cac gag gtg gac cac	528
Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His	
165 170 175	
ttc ctg cgt gag atg ccc gcc ctg atc cgg atg gcc tgc gtc agc act	576
Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr	
180 185 190	
gtg gcc atc gaa ggc acc gtc ttt gtc ctg aaa aaa ggt gtt gtg ctg	624
Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu	
195 200 205	
tcc ccc ttg gtg ttt atc ctg ctc tct tac agc tac att gtg agg gct	672
Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala	
210 215 220	
gtg tta caa att cgg tca gca tca gga agg cag aag gcc ttc ggc acc	720
Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr	
225 230 235 240	
tgc ggc tcc cat ctc act gtg gtc tcc ctt ttc tat gga aac atc atc	768
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile	
245 250 255	

82/261

tac atg tac atg cag cca gga gcc agt tct tcc cag gac cag ggc atg 816  
 Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met  
                   260                  265                  270  
  
 ttc ctc atg ctc ttc tac aac att gtc acc ccc ctc ctc aat cct ctc 864  
 Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu  
                   275                  280                  285  
  
 atc tac acc ctc aga aac aga gag gtg aag ggg gca ctg gga agg ttg 912  
 Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu  
                   290                  295                  300  
  
 ctt ctg ggg aag aga gag cta gga aag gag 942  
 Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu  
                   305                  310

<210> 72  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly  
   1                  5                  10                  15  
 Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu  
                   20                  25                  30  
 Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val  
                   35                  40                  45  
 Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
                   50                  55                  60  
 His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln  
   65                  70                  75                  80  
 Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly  
                   85                  90                  95  
 Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys  
                   100                  105                  110  
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys  
                   115                  120                  125  
 Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu  
                   130                  135                  140  
 Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser  
   145                  150                  155                  160  
 Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His  
                   165                  170                  175  
 Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr  
                   180                  185                  190  
 Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu  
                   195                  200                  205  
 Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala  
                   210                  215                  220  
 Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr  
   225                  230                  235                  240  
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile  
                   245                  250                  255  
 Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met  
                   260                  265                  270  
 Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu  
                   275                  280                  285  
 Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu  
                   290                  295                  300



83/261

Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu  
305 310

<210> 73  
<211> 942  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(942)

<400> 73  
atg tcc aga aga aac tat act gaa ctg aca gaa ttt gtt ctc ttg ggt 48  
Met Ser Arg Arg Asn Tyr Thr Glu Leu Thr Glu Phe Val Leu Leu Gly  
1 5 10 15  
cta aca agc cgt cca gag ctg cga gcc ccg tgc ttt ggg gtg ttt tta 96  
Leu Thr Ser Arg Pro Glu Leu Arg Ala Pro Cys Phe Gly Val Phe Leu  
20 25 30  
gtt atc tat ctg gtc aca gtg ctg ggc aat ctt ggg ttg att act tta 144  
Val Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu  
35 40 45  
atc aag att gat act cga ctc cac aca cct atg tac tat ttc ctc agc 192  
Ile Lys Ile Asp Thr Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
50 55 60  
cac ctg gcc ttt gtt gac ctt tgt tac tcc tct gct att aca ccg aag 240  
His Leu Ala Phe Val Asp Leu Cys Tyr Ser Ser Ala Ile Thr Pro Lys  
65 70 75 80  
atg atg gtg aat ttt gtt gtg gaa cgc aac acc att cct ttc cat gct 288  
Met Met Val Asn Phe Val Val Glu Arg Asn Thr Ile Pro Phe His Ala  
85 90 95  
tgt gca acc caa ctg ggt tgt ttt ctc acc ttc atg atc act gag tgt 336  
Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr Phe Met Ile Thr Glu Cys  
100 105 110  
ttc ctt cta gcc tcc atg gcc tac gat tgc tat gtc gcc atc tgt agt 384  
Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Ser  
115 120 125  
ccc ctg cat tat tca aca ctg atg tca aga aga gtc tgc att caa ctg 432  
Pro Leu His Tyr Ser Thr Leu Met Ser Arg Arg Val Cys Ile Gln Leu  
130 135 140  
gtg gca gtt cca tat ata tac agc ttc ctg gtt gcc ctc ttc cac acc 480  
Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu Val Ala Leu Phe His Thr  
145 150 155 160  
gtt atc act ttc cgt ctg act tac tgt ggc cca aac tta att aac cat 528  
Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly Pro Asn Leu Ile Asn His  
165 170 175  
ttc tat tgt gat gac ctc ccc ttc tta gct ctg tcc tgc tca gac aca 576  
Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala Leu Ser Cys Ser Asp Thr  
180 185 190

84/261

cac atg aag gaa att ctg ata ttt gcc ttt gct ggc ttt gat atg atc 624  
 His Met Lys Glu Ile Leu Ile Phe Ala Phe Ala Gly Phe Asp Met Ile  
 195 200 205  
 tct tcc tct tcc att gtc ctc acc tcc tac atc ttt att att gcc gct 672  
 Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr Ile Phe Ile Ile Ala Ala  
 210 215 220  
 atc cta agg atc cgc tct act cag ggg caa cac aaa gcc att tcc acc 720  
 Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln His Lys Ala Ile Ser Thr  
 225 230 235 240  
 tgt ggc tcc cat atg gtg act gtc act att ttc tat ggc aca ctg atc 768  
 Cys Gly Ser His Met Val Thr Val Thr Ile Phe Tyr Gly Thr Leu Ile  
 245 250 255  
 ttt atg tac cta cag ccc aaa tca aat cac tcc ttg gac aca gac aag 816  
 Phe Met Tyr Leu Gln Pro Lys Ser Asn His Ser Leu Asp Thr Asp Lys  
 260 265 270  
 atg gct tct gta ttt tac aca gtg gtg atc ccc atg tta aac ccc cta 864  
 Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 atc tat agt cta agg aac aaa gaa gtg aaa gat gcc tca aag aaa gcc 912  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ser Lys Lys Ala  
 290 295 300  
 ttg gat aaa ggt tgt gaa aac tta cag ata 942  
 Leu Asp Lys Gly Cys Glu Asn Leu Gln Ile  
 305 310

&lt;210&gt; 74

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

Met Ser Arg Arg Asn Tyr Thr Glu Leu Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Thr Ser Arg Pro Glu Leu Arg Ala Pro Cys Phe Gly Val Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Ile Lys Ile Asp Thr Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 His Leu Ala Phe Val Asp Leu Cys Tyr Ser Ser Ala Ile Thr Pro Lys  
 65 70 75 80  
 Met Met Val Asn Phe Val Val Glu Arg Asn Thr Ile Pro Phe His Ala  
 85 90 95  
 Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr Phe Met Ile Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu His Tyr Ser Thr Leu Met Ser Arg Arg Val Cys Ile Gln Leu  
 130 135 140  
 Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu Val Ala Leu Phe His Thr  
 145 150 155 160  
 Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly Pro Asn Leu Ile Asn His  
 165 170 175

85/261

Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 His Met Lys Glu Ile Leu Ile Phe Ala Phe Ala Gly Phe Asp Met Ile  
 195 200 205  
 Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr Ile Phe Ile Ile Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln His Lys Ala Ile Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Met Val Thr Val Thr Ile Phe Tyr Gly Thr Leu Ile  
 245 250 255  
 Phe Met Tyr Leu Gln Pro Lys Ser Asn His Ser Leu Asp Thr Asp Lys  
 260 265 270  
 Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ser Lys Lys Ala  
 290 295 300  
 Leu Asp Lys Gly Cys Glu Asn Leu Gln Ile  
 305 310

&lt;210&gt; 75

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(945)

&lt;400&gt; 75

atg act ctg aga aac agc tcc tca gtg act gag ttt atc ctt gtg gga 48  
 Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly  
 1 5 10 15  
 tta tca gaa cag cca gag ctc cag ctc cct ctt ttc ctt cta ttc tta 96  
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 ggg atc tat gtg ttc act gtg gtg ggc aac ttg ggc ttg atc acc tta 144  
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 att ggg ata aat cct agc ctt cac acc ccc atg tac ttt ttc ctc ttc 192  
 Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 aac ttg tcc ttt ata gat ctc tgt tat tcc tgt gtg ttt acc ccc aaa 240  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys  
 65 70 75 80  
 atg ctg aat gac ttt gtt tca gaa agt atc atc tct tat gtg gga tgt 288  
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys  
 85 90 95  
 atg act cag cta ttt ttc ttc tgt ttc ttt gtc aat tct gag tgc tat 336  
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr  
 100 105 110  
 gtg ttg gta tca atg gcc tat gat cgc tat gtg gcc atc tgc aac ccc 384  
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125

86/261

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ctg ctc tac atg gtc acc atg tcc cca agg gtc tgc ttt ctg ctg atc 432
Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Ile
130 135 140

ctt atg ttt ggt tcc tat ttg atg gcc ttt tct ggt gcc atg gcc cac 480
Leu Met Phe Gly Ser Tyr Leu Met Ala Phe Ser Gly Ala Met Ala His
145 150 155 160

act gga tgc atg ctg aga ctg act ttc tgt gat gcg aac acc atc gat 528
Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp
165 170 175

cac tac ttc tgt gac atc ctc cct ctg ctc cag ctc tcc tgc acc agc 576
His Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser
180 185 190

acc tac atc aat gag ctg gtg gtt ttc act gtg gtt ggc atc aac atc 624
Thr Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile
195 200 205

att gtg ccc act gtt acc atc ttt atc tct tat ggt ttc atc ctc tcc 672
Ile Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
210 215 220

agc atc ctc cat atc agt tcc aag gag ggc agg tcc aaa gct ttc agc 720
Ser Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser
225 230 235 240

act tgc agt tcc cat ata att gct gtt tct ctg ttc ttt gga tca ggt 768
Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
245 250 255

gca ttt atg tat ctc aac cca tct tct gct ggg tcc atg gat aag aga 816
Ala Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg
260 265 270

aaa tta tct tct gtc ttt tat aca aat gtg gtt ccc atg ttg aac ccc 864
Lys Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro
275 280 285

tta atc tac agc ctg agg aac aaa gat gtt aaa ttt gcc cta aga aaa 912
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys
290 295 300

gcc ctg aga cga agg cat aag tta tct gat att 945
Ala Leu Arg Arg Arg His Lys Leu Ser Asp Ile
305 310 315

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<210> 76  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
 Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly  
 1 5 10 15  
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45

87/261

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Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
  50          55          60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
  65          70          75          80
Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
          85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
          100          105          110
Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Ile
          130          135          140
Leu Met Phe Gly Ser Tyr Leu Met Ala Phe Ser Gly Ala Met Ala His
          145          150          155          160
Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp
          165          170          175
His Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser
          180          185          190
Thr Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile
          195          200          205
Ile Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
          210          215          220
Ser Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser
          225          230          235          240
Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
          245          250          255
Ala Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg
          260          265          270
Lys Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys
          290          295          300
Ala Leu Arg Arg Arg His Lys Leu Ser Asp Ile
          305          310          315

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<210> 77  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

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<400> 77
atg tgg atc aac aat caa agc tcg cta gat gat ttt atc cta ttg gga 48
Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
  1          5          10          15

ttt tct gac cgt ccc tgg cta gag aca ccc ctc tct gta atc ttt ctg 96
Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Ser Val Ile Phe Leu
          20          25          30

gtg gcc tac atc ttt tcc cta ttt gga aat atc tcc att atc cta gtt 144
Val Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val
          35          40          45

tcc cat ctg gat ccc cag ctt gac agt ccc atg tac ttt ttt gtc tct 192
Ser His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser
          50          55          60

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88/261

aat cta tcc ttt ctg gac ctc tgc tat acc acc agc act gtc cca cag	240
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln	
65 70 75 80	
atg ctg gtc aac ctc cgg gga cca gaa aag acc att agc tat ggg ggt	288
Met Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly	
85 90 95	
tgt gtt gcc caa ctc tat ata ttt ttg gcc ctg ggt tct act gaa tgc	336
Cys Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys	
100 105 110	
ata ctt cta gcc atc atg gcc ttt gac cgt tac gct gcc ata tgc aag	384
Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys	
115 120 125	
ccc ctt cac tac cca gtc atc atg aac cat aga cgc tgt atc cac atg	432
Pro Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met	
130 135 140	
gct gct ggc act tgg atc agt ggc ttt gct aac tcc ctt gtc cag tcc	480
Ala Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser	
145 150 155 160	
act ctc aca gtg gtg gcc cca aga tgt gga cag agg gtg ttg gac cat	528
Thr Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His	
165 170 175	
ttc ttc tgt gaa gtt cca gcc ctt ttg aaa cta gcc tgt att gat att	576
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile	
180 185 190	
cgt gtg aat gaa atg gag ctc aat gta cta ggc gct ttg ctt ctc ctg	624
Arg Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu	
195 200 205	
atg cca ctc acc ctc atc ctg ggc act tat gtg ttc att gct cag gca	672
Met Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala	
210 215 220	
gta atg aga atc tgc tct gct gaa agt cgc tgg aag gct ttc aat acc	720
Val Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr	
225 230 235 240	
tgt gcc tca cat ttg ctg gtg gtc tcc ctc ttc tac ttc aca gcc atc	768
Cys Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile	
245 250 255	
agt atg tat gtc cag cct ccc tct agc tat tct cat gac cgg ggg aag	816
Ser Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys	
260 265 270	
atc atg gct ctc ttt tat ggc att gtc aca ccc acc ctc aac cca ttc	864
Ile Met Ala Leu Phe Tyr Gly Ile Val Thr Pro Thr Leu Asn Pro Phe	
275 280 285	
atc tac aca ttg aga aac aag gat gtg aaa gct gcc ctg aga agg tca	912
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Arg Ser	
290 295 300	

89/261

ctg act aaa gag ttt tgg att aag aca aga  
 Leu Thr Lys Glu Phe Trp Ile Lys Thr Arg  
 305 310

942

<210> 78  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
 Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Ser Val Ile Phe Leu  
 20 25 30  
 Val Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val  
 35 40 45  
 Ser His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly  
 85 90 95  
 Cys Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met  
 130 135 140  
 Ala Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser  
 145 150 155 160  
 Thr Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His  
 165 170 175  
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile  
 180 185 190  
 Arg Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu  
 195 200 205  
 Met Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala  
 210 215 220  
 Val Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile  
 245 250 255  
 Ser Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys  
 260 265 270  
 Ile Met Ala Leu Phe Tyr Gly Ile Val Thr Pro Thr Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Arg Ser  
 290 295 300  
 Leu Thr Lys Glu Phe Trp Ile Lys Thr Arg  
 305 310

<210> 79  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

90/261

<400> 79  
 atg ggt aga aga aat aac aca aat gtg cct gac ttc atc ctt acg gga 48  
 Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly  
 1 5 10 15

ctg tca gat tct gaa gag gtc cag atg gcc ctc ttt ata cta ttt ctc 96  
 Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu  
 20 25 30

ctg ata tac cta att act atg ctg ggc aat gtg ggg atg ata ttg ata 144  
 Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile  
 35 40 45

atc cgc ctg gac ctc cag ctt cac act ccc atg tat ttt ttc ctt act 192  
 Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60

cac ttg tca ttt att gac ctc agt tac tca act gtc atc aca cct aaa 240  
 His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys  
 65 70 75 80

acc tta gcg aac tta ctg act tcc aac tat att tcc ttc atg ggc tgc 288  
 Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys  
 85 90 95

ttt gcc cag atg ttc ttt ttt gtc ttc ttg gga gct gct gaa tgt ttt 336  
 Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe  
 100 105 110

ctt ctc tca tca atg gcc tat gat cgc tac gta gct atc tgc agt cct 384  
 Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro  
 115 120 125

cta cgt tac cca gtt att atg tcc aaa agg ctg tgt tgc gct ctt gtc 432  
 Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val  
 130 135 140

act ggg ccc tat gtg att agc ttt atc aac tcc ttt gtc aat gtg gtt 480  
 Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val  
 145 150 155 160

tgg atg agc aga ctg cat ttc tgc gac tca aat gta gtt cgt cac ttt 528  
 Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe  
 165 170 175

ttc tgc gac acg tct cca att tta gct ctg tcc tgc atg gac aca tac 576  
 Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr  
 180 185 190

gac att gaa atc atg ata cac att tta gct ggt tcc acc ctg atg gtg 624  
 Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val  
 195 200 205

tcc ctt atc aca ata tct gca tcc tat gtg tcc att ctc tct acc atc 672  
 Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile  
 210 215 220

ctg aaa att aat tcc act tca gga aag cag aaa gct ttg tct act tgt 720  
 Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys  
 225 230 235 240



91/261

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gcc tct cat ctc ttg gga gtc acc atc ttt tat gga act atg att ttt 768
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
                245                250                255

act tat tta aaa cca aga aag tct tat tct ttg gga agg gat caa gtg 816
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
                260                265                270

gct tct gtt ttt tat act att gtg att ccc atg ctg aat cca ctc att 864
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
                275                280                285

tat agt ctt aga aac aaa gaa gtt aaa aat gct ctc att aga gtc atg 912
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
                290                295                300

cag aga aga cag gac tcc agt cag tgg 939
Gln Arg Arg Gln Asp Ser Ser Gln Trp
305                310

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<210> 80  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

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<400> 80
Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1          5          10          15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
 20          25          30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
 35          40          45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
 65          70          75          80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
 85          90          95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
260          265          270

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92/261

Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile  
           275                          280                          285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met  
           290                          295                          300  
 Gln Arg Arg Gln Asp Ser Ser Gln Trp  
 305                          310

<210> 81  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 81  
 atg ttg tcc cca aac cac acc ata gtg aca gaa ttc att ctc tta gga 48  
 Met Leu Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly  
   1                          5                          10                          15  
 ctg aca gac gac cca gtg cta gag aag atc ctg ttt ggg gtg ttc ctg 96  
 Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu  
                           20                          25                          30  
 gcg atc tac cta atc aca ctg gca ggc aac ctg tgc atg atc ctg ctg 144  
 Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu  
                           35                          40                          45  
 atc agg acc aat tcc caa ctg caa aca ccc atg tat ttc ttc ctt ggt 192  
 Ile Arg Thr Asn Ser Gln Gln Thr Pro Met Tyr Phe Phe Leu Gly  
           50                          55                          60  
 cac ctc tcc ttt gta gac att tgc tat tct tcc aat gtt act cca aat 240  
 His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn  
   65                          70                          75                          80  
 atg ctg cac aat ttc ctc tca gaa cag aag acc atc tcc tac gct gga 288  
 Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly  
                           85                          90                          95  
 tgc ttc aca cag tgt ctt ctc ttc atc gcc cta gtg atc act gag ttt 336  
 Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe  
                           100                          105                          110  
 tac ttc ctt gct tca atg gca ttg gat cgc tat gta gcc att tgc agc 384  
 Tyr Phe Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser  
           115                          120                          125  
 cct tta cat tac agt tcc agg atg tcc aag aac att tgc atc tct ctg 432  
 Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Ile Ser Leu  
   130                          135                          140  
 gtc act gtg cct tac atg tat ggc ttc ctt aat ggg ctc tct cag aca 480  
 Val Thr Val Pro Tyr Met Tyr Gly Phe Leu Asn Gly Leu Ser Gln Thr  
   145                          150                          155                          160  
 ctg ctg acc ttt cac tta tcc ttc tgt ggc tcc ctt gaa atc aat cat 528  
 Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His  
                           165                          170                          175

93/261

ttc tac tgc gct gat cct cct ctt atc atg ctg gcc tgc tct gac acc 576  
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr  
 180 185 190

cgt gtc aaa aag atg gca atg ttt gta gtt gca ggc ttt act ctc tca 624  
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Thr Leu Ser  
 195 200 205

agc tct ctc ttc atc att ctt ctg tcc tat ctt ttc att ttt gca gcg 672  
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala  
 210 215 220

atc ttc agg atc cgt tct gct gaa ggc agg cac aaa gcc ttt tct acg 720  
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240

tgt gct tcc cac ctg aca ata gtc act ttg ttt tat gga acc ctc ttc 768  
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe  
 245 250 255

tgc atg tac gta agg cct cca tca gag aag tca gtg gaa cag tcc aaa 816  
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Gln Ser Lys  
 260 265 270

gtc att gct gtt ttc tac act ttt gta agc cct atg ttg aac ccc atc 864  
 Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro Ile  
 275 280 285

atc tat agt ttg agg aac aag gat gtg aaa caa gct ttt tgg aaa ctg 912  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys Leu  
 290 295 300

atc aga aga aac cag att tgt ttt ctc tgg 942  
 Ile Arg Arg Asn Gln Ile Cys Phe Leu Trp  
 305 310

&lt;210&gt; 82

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 82

Met Leu Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu  
 20 25 30  
 Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu  
 35 40 45  
 Ile Arg Thr Asn Ser Gln Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn  
 65 70 75 80  
 Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe  
 100 105 110  
 Tyr Phe Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Ile Ser Leu  
 130 135 140

94/261

Val Thr Val Pro Tyr Met Tyr Gly Phe Leu Asn Gly Leu Ser Gln Thr  
 145 150 155 160  
 Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His  
 165 170 175  
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Thr Leu Ser  
 195 200 205  
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala  
 210 215 220  
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe  
 245 250 255  
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Gln Ser Lys  
 260 265 270  
 Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys Leu  
 290 295 300  
 Ile Arg Arg Asn Gln Ile Cys Phe Leu Trp  
 305 310

<210> 83  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (948)

<400> 83  
 atg ggg gga aat cag act tcc atc aca gag ttc ctc cta ctg gga ttt 48  
 Met Gly Gly Asn Gln Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe  
 1 5 10 15  
 ccc att ggc cca agg att cag atg ctc ctc ttt ggg ctc ttc tcc ctg 96  
 Pro Ile Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20 25 30  
 ttc tac atc ttc att ctc tta acc ctg atg gga aat ggg att atc ctg 144  
 Phe Tyr Ile Phe Ile Leu Leu Thr Leu Met Gly Asn Gly Ile Ile Leu  
 35 40 45  
 ggg ctc atc tac ttg gac tct aga ctg cac aca ccc atg tat gtc ttc 192  
 Gly Leu Ile Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe  
 50 55 60  
 ctg tca cac ctg gcc att gtg gac atg tcc tat gcc tcg agt act gtc 240  
 Leu Ser His Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val  
 65 70 75 80  
 cct aag atg cta gca aat ctt gtg atg cac aaa aaa gtc atc tcc ttt 288  
 Pro Lys Met Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe  
 85 90 95  
 gct cct tgc ata ctt cag act ttt ttg tat ttg gcg ttt gct att aca 336  
 Ala Pro Cys Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr  
 100 105 110

95/261

gag tgt ctg att ttg gtg atg atg tgc tat gat cgg tat gtg gca atc 384  
 Glu Cys Leu Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile  
 115 120 125

tgt cac ccc ttg caa tac acc ctc att atg aac tgg aga gtg tgc act 432  
 Cys His Pro Leu Gln Tyr Thr Leu Ile Met Asn Trp Arg Val Cys Thr  
 130 135 140

gtc ctg gcc tca act tgc tgg ata ttt agc ttt ctc ttg gct ctg gtc 480  
 Val Leu Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala Leu Val  
 145 150 155 160

cat att act ctt att ctg agg ctg cct ttt tgt ggc cca caa aag atc 528  
 His Ile Thr Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Lys Ile  
 165 170 175

aac cac ttt ttc tgt caa atc atg tcc gta ttc aaa ttg gcc tgt gct 576  
 Asn His Phe Phe Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala  
 180 185 190

gac act agg ctc aac cag gtg gtc cta ttt gcg ggt tct gcg ttc atc 624  
 Asp Thr Arg Leu Asn Gln Val Val Leu Phe Ala Gly Ser Ala Phe Ile  
 195 200 205

tta gtg ggg ccg ctc tgc ctg gtg ctg gtc tcc tac ttg cac atc ctg 672  
 Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu  
 210 215 220

gtg gcc atc ttg agg atc cag tct ggg gag ggc cgc aga aag gcc ttc 720  
 Val Ala Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe  
 225 230 235 240

tct acc tgc tcc tcc cac ctc tgc gtg gtg ggg ctt ttc ttt ggc agc 768  
 Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser  
 245 250 255

gcc att gtc atg tac atg gcc ccc aag tca agc cat tct caa gaa cgg 816  
 Ala Ile Val Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg  
 260 265 270

agg aag atc ctt tcc ctg ttt tac agc ctt ttc aac ccg atc ctg aac 864  
 Arg Lys Ile Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn  
 275 280 285

ccc ctc atc tac agc ctt agg aat gca gag gtg aaa ggg gct cta aag 912  
 Pro Leu Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys  
 290 295 300

aga gtc ctt tgg aaa cag aga tca ata agt tat tgg 948  
 Arg Val Leu Trp Lys Gln Arg Ser Ile Ser Tyr Trp  
 305 310 315

<210> 84  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Gly Gly Asn Gln Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe  
 1 5 10 15

96/261

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Pro Ile Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20      25      30
Phe Tyr Ile Phe Ile Leu Leu Thr Leu Met Gly Asn Gly Ile Ile Leu
      35      40      45
Gly Leu Ile Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe
      50      55      60
Leu Ser His Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val
      65      70      75      80
Pro Lys Met Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe
      85      90      95
Ala Pro Cys Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr
      100      105      110
Glu Cys Leu Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile
      115      120      125
Cys His Pro Leu Gln Tyr Thr Leu Ile Met Asn Trp Arg Val Cys Thr
      130      135      140
Val Leu Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala Leu Val
      145      150      155      160
His Ile Thr Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Lys Ile
      165      170      175
Asn His Phe Phe Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala
      180      185      190
Asp Thr Arg Leu Asn Gln Val Val Leu Phe Ala Gly Ser Ala Phe Ile
      195      200      205
Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu
      210      215      220
Val Ala Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe
      225      230      235      240
Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser
      245      250      255
Ala Ile Val Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg
      260      265      270
Arg Lys Ile Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys
      290      295      300
Arg Val Leu Trp Lys Gln Arg Ser Ile Ser Tyr Trp
      305      310      315

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&lt;210&gt; 85

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(954)

&lt;400&gt; 85

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atg gct ggc aac aat ttc act gag gtt acc gtc ttc atc ctc tct gga 48
Met Ala Gly Asn Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
  1          5          10          15

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ttt gca aat cac cct gaa tta caa gtc agt ctt ttc ttg atg ttt ctc 96
Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu
      20          25          30

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```

ttc att tat cta ttc act gtt ttg gga aac ctg gga ctg atc acg tta 144
Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
      35          40          45

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97/261

atc aga atg gat tct cag ctt cac acc cct atg tac ttt ttc ctg agc	192
Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
aat tta gca ttt att gac ata ttt tac tcc tct act gta aca cct aag	240
Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys	
65 70 75 80	
gca ttg gtg aat ttc caa tcc aat cgg aga tcc atc tcc ttt gtt ggc	288
Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly	
85 90 95	
tgc ttt gtt caa atg tac ttt ttt atg ttc tgt ttt gtc ttc ttg ggt	336
Cys Phe Val Gln Met Tyr Phe Phe Met Phe Cys Phe Val Leu Gly	
100 105 110	
act gct gaa tgt tat ctt ctc tcc tca atg gcc tat gat cgc tat gca	384
Thr Ala Glu Cys Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala	
115 120 125	
gcg atc tgc agt cct cta cac tac aca gtt att atg ccc aaa agg ctc	432
Ala Ile Cys Ser Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu	
130 135 140	
tgc ctc gct ctc atc act ggg cct tat gtg att ggc ttt atg gac tcc	480
Cys Leu Ala Leu Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser	
145 150 155 160	
ttt gtc aat gtg gtt tcc atg agc aga ttg cat ttc tgt gac tca aac	528
Phe Val Asn Val Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn	
165 170 175	
ata att cat cac ttt ttc tgt gac act tcc cca att tta gct ctg tcc	576
Ile Ile His His Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser	
180 185 190	
tgc act gac aca gac aac act gaa atg ctg ata ttc att atc gct ggt	624
Cys Thr Asp Thr Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly	
195 200 205	
tcc acc ctg atg gtg tcc ctt atc aca ata tct gca tcc tat gtg tcc	672
Ser Thr Leu Met Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser	
210 215 220	
att ctc tct acc atc ctg aaa att aat tcc act tca gga aag cag aaa	720
Ile Leu Ser Thr Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys	
225 230 235 240	
gct ttc tct act tgc gtc tct cat ctc ttg gga gtc acc atc ttc tat	768
Ala Phe Ser Thr Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr	
245 250 255	
gga act atg att ttt act tac tta aag cca aga aag tct tat tcc ttg	816
Gly Thr Met Ile Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu	
260 265 270	
gga aga gat caa gtg gct cct gtg ttt tat act att gtg att ccc atg	864
Gly Arg Asp Gln Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met	
275 280 285	
ctg aat cca ctc att tat agt ctt aga aac aga gaa gtg aaa aat gct	912

98/261

Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala  
 290 295 300

ctc att aga gtc atg cag aga aga cag gac tcc aga aaa tgg 954  
 Leu Ile Arg Val Met Gln Arg Arg Gln Asp Ser Arg Lys Trp  
 305 310 315

<210> 86  
 <211> 318  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Met Ala Gly Asn Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly  
 1 5 10 15  
 Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu  
 20 25 30  
 Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Phe Val Gln Met Tyr Phe Phe Met Phe Cys Phe Val Phe Leu Gly  
 100 105 110  
 Thr Ala Glu Cys Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala  
 115 120 125  
 Ala Ile Cys Ser Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu  
 130 135 140  
 Cys Leu Ala Leu Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser  
 145 150 155 160  
 Phe Val Asn Val Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn  
 165 170 175  
 Ile Ile His His Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser  
 180 185 190  
 Cys Thr Asp Thr Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly  
 195 200 205  
 Ser Thr Leu Met Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser  
 210 215 220  
 Ile Leu Ser Thr Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr  
 245 250 255  
 Gly Thr Met Ile Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu  
 260 265 270  
 Gly Arg Asp Gln Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met  
 275 280 285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala  
 290 295 300  
 Leu Ile Arg Val Met Gln Arg Arg Gln Asp Ser Arg Lys Trp  
 305 310 315

<210> 87  
 <211> 933  
 <212> DNA  
 <213> Homo sapiens



99/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(933)

&lt;400&gt; 87

atg gca gca gaa aac cat tct ttt gtg act aag ttt att ctg gtt ggg	48
Met Ala Ala Glu Asn His Ser Phe Val Thr Lys Phe Ile Leu Val Gly	
1 5 10 15	
cta aca gag aag tca gag cta cag ctg ccc ctc ttc ctc gtc ttc ctg	96
Leu Thr Glu Lys Ser Glu Leu Gln Leu Pro Leu Phe Leu Val Phe Leu	
20 25 30	
gga atc tat gta gtc aca gtg ctg ggg aac ctg ggc atg atc aca ctg	144
Gly Ile Tyr Val Val Thr Val Leu Gly Asn Leu Gly Met Ile Thr Leu	
35 40 45	
att ggg ctc agt tct cac ctg cac aca cct atg tac tgt ttc ctc agc	192
Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr Cys Phe Leu Ser	
50 55 60	
agt ctg tcc ttc att gac ttc tgc cat tcc act gtc att acc cct aag	240
Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val Ile Thr Pro Lys	
65 70 75 80	
atg ctg gtg aac ttt gtg aca gag aag aac atc atc tcc tac cct gaa	288
Met Leu Val Asn Phe Val Thr Glu Lys Asn Ile Ile Ser Tyr Pro Glu	
85 90 95	
tgc atg act cag ctc tac ttc ttc ctc gtt ttt gct att gca gag tgt	336
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Phe Ala Ile Ala Glu Cys	
100 105 110	
cac atg ttg gct gca atg gca tat gac ggc tac gtg gcc atc tgt agc	384
His Met Leu Ala Ala Met Ala Tyr Asp Gly Tyr Val Ala Ile Cys Ser	
115 120 125	
ccc ttg ctg tac agc atc atc ata tcc aat aag gct tgc ttt tct ctg	432
Pro Leu Leu Tyr Ser Ile Ile Ile Ser Asn Lys Ala Cys Phe Ser Leu	
130 135 140	
att tta gtg gtg tat gta ata ggc ctg att tgt gcg tca gct cat ata	480
Ile Leu Val Val Tyr Val Ile Gly Leu Ile Cys Ala Ser Ala His Ile	
145 150 155 160	
ggc tgt atg ttt agg gtt caa ttc tgc aaa ttt gat gtg atc aac cat	528
Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Val Ile Asn His	
165 170 175	
tat ttc tgt gat ctt att tct atc ttg aag ctc tcc tgt tct agt act	576
Tyr Phe Cys Asp Leu Ile Ser Ile Leu Lys Leu Ser Cys Ser Ser Thr	
180 185 190	
tac att aat gag tta ctg att tta atc ttt agt gga att aac atc ctt	624
Tyr Ile Asn Glu Leu Leu Ile Leu Ile Phe Ser Gly Ile Asn Ile Leu	
195 200 205	
gtc ccc agc ctg acc atc ctc agc tct tac atc ttc atc att gcc agc	672
Val Pro Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser	
210 215 220	

100/261

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atc ctc cgc att cgc tac act gag ggc agg tcc aaa gcc ttc agc act 720
Ile Leu Arg Ile Arg Tyr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
225                230                235                240

tgc agc tcc cac atc tcg gct gtt tct gtt ttc ttt ggg tct gca gca 768
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
                245                250                255

ttc atg tac ctg cag cca tca tct gtc agc tcc atg gac cag ggg aaa 816
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
                260                265                270

gtg tcc tct gtg ttt tat act att gtt gtg ccc atg ctg aac ccc ctg 864
Val Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Leu Asn Pro Leu
                275                280                285

atc tac agc ctg agg aat aaa gat gtc cac gtt gcc ctg aag aaa acg 912
Ile Tyr Ser Leu Arg Asn Lys Asp Val His Val Ala Leu Lys Lys Thr
                290                295                300

cta ggg aaa aga aca ttc tta 933
Leu Gly Lys Arg Thr Phe Leu
305                310

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<210> 88  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

```

<400> 88
Met Ala Ala Glu Asn His Ser Phe Val Thr Lys Phe Ile Leu Val Gly
 1          5          10          15
Leu Thr Glu Lys Ser Glu Leu Gln Leu Pro Leu Phe Leu Val Phe Leu
 20          25          30
Gly Ile Tyr Val Val Thr Val Leu Gly Asn Leu Gly Met Ile Thr Leu
 35          40          45
Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr Cys Phe Leu Ser
 50          55          60
Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val Ile Thr Pro Lys
 65          70          75          80
Met Leu Val Asn Phe Val Thr Glu Lys Asn Ile Ile Ser Tyr Pro Glu
 85          90          95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Phe Ala Ile Ala Glu Cys
100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp Gly Tyr Val Ala Ile Cys Ser
115          120          125
Pro Leu Leu Tyr Ser Ile Ile Ser Asn Lys Ala Cys Phe Ser Leu
130          135          140
Ile Leu Val Val Tyr Val Ile Gly Leu Ile Cys Ala Ser Ala His Ile
145          150          155          160
Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Val Ile Asn His
165          170          175
Tyr Phe Cys Asp Leu Ile Ser Ile Leu Lys Leu Ser Cys Ser Ser Thr
180          185          190
Tyr Ile Asn Glu Leu Leu Ile Leu Ile Phe Ser Gly Ile Asn Ile Leu
195          200          205
Val Pro Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser
210          215          220
Ile Leu Arg Ile Arg Tyr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240

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[illegible]

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<220>  
<221> CDS  
<222> (1) ... (939)
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<400> 89																	
atg	act	ctg	aga	aac	agc	tcc	tca	gtg	act	gag	ttt	atc	ctt	gtg	gga	48	
Met	Thr	Leu	Arg	Asn	Ser	Ser	Ser	Val	Thr	Glu	Phe	Ile	Leu	Val	Gly		
1		5			10					15							
tta	tca	gaa	cag	cca	gag	ctc	cag	ctc	cct	ctt	ttc	ctt	cta	ttc	tta	96	
Leu	Ser	Glu	Gln	Pro	Glu	Leu	Gln	Leu	Pro	Leu	Phe	Leu	Leu	Phe	Leu		
20			25					30									
ggg	atc	tat	gtg	ttc	act	gtg	gtg	ggc	aac	ttg	ggc	ttg	atc	acc	tta	144	
Gly	Ile	Tyr	Val	Phe	Thr	Val	Val	Gly	Asn	Leu	Gly	Leu	Ile	Thr	Leu		
35			40					45									
att	ggg	ata	aat	cct	agc	ctt	cac	acc	ccc	atg	tac	ttt	ttc	ctc	ttc	192	
Ile	Gly	Ile	Asn	Pro	Ser	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe		
50		55					60										
aac	ttg	tcc	ttt	ata	gat	ctc	tgt	tat	tcc	tgt	gtg	ttt	acc	ccc	aaa	240	
Asn	Leu	Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Cys	Val	Phe	Thr	Pro	Lys		
65		70					75					80					
atg	ctg	aat	gac	ttt	gtt	tca	gaa	agt	atc	atc	tct	tat	gtg	gga	tgt	288	
Met	Leu	Asn	Asp	Phe	Val	Ser	Glu	Ser	Ile	Ile	Ser	Tyr	Val	Gly	Cys		
85				90					95								
atg	act	cag	cta	ttt	ttc	ttc	tgt	ttc	ttt	gtc	aat	tct	gag	tgc	tat	336	
Met	Thr	Gln	Leu	Phe	Phe	Phe	Cys	Phe	Phe	Val	Asn	Ser	Glu	Cys	Tyr		
100			105					110									
gtg	ttg	gta	tca	atg	gcc	tat	gat	cgc	tat	gtg	gcc	atc	tgc	aac	ccc	384	
Val	Leu	Val	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro		
115			120					125									
ctg	ctc	tac	atg	gtc	acc	atg	tcc	cca	agg	gtc	tgc	ttt	ctg	ctg	atg	432	
Leu	Leu	Tyr	Met	Val	Thr	Met	Ser	Pro	Arg	Val	Cys	Phe	Leu	Leu	Met		
130			135					140									
ttt	ggg	tcc	tat	gtg	gta	ggg	ttt	gct	ggg	gcc	atg	gcc	cac	act	gga	480	
Phe	Gly	Ser	Tyr	Val	Val	Gly	Phe	Ala	Gly	Ala	Met	Ala	His	Thr	Gly		
145		150					155					160					

102/261

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agc atg ctg cga ctg acc ttc tgt gat tcc aac gtc att gac cat tat 528
Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
165 170 175

ctg tgt gac gtt ctc ccc ctc ttg cag ctc tcc tgc acc agc acc cat 576
Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
180 185 190

gtc agt gag ctg gtg gtt gtt ctc att gtt gtg ggt att aat atc atg 624
Val Ser Glu Leu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
195 200 205

gta ccc agt tgt acc atc ctc att tct tat gtt ttc att gtc act agc 672
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210 215 220

att ctt cat atc aaa tcc act caa gga aga tca aaa gcc ttc agt act 720
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225 230 235 240

tgt agc tct cat gtc att gct ctg tct ctg ttt ttt ggg tca gcg gca 768
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245 250 255

ttc atg tat att aaa tat tct tct gga tct atg gag cag gga aaa gtt 816
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
260 265 270

tct tct gtt ttc tac act aat gtg gtg ccc atg ctc aat cct ctc atc 864
Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
275 280 285

tac agt ttg agg aac aag gat gtc aaa gtt gca ctg agg aaa gct ctg 912
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
290 295 300

att aaa att cag aga aga aat ata ttc 939
Ile Lys Ile Gln Arg Arg Asn Ile Phe
305 310

```

&lt;210&gt; 90

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
1 5 10 15
Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20 25 30
Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
35 40 45
Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
50 55 60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
65 70 75 80
Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
85 90 95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
100 105 110

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103/261

Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met  
 130 135 140  
 Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly  
 145 150 155 160  
 Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr  
 165 170 175  
 Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His  
 180 185 190  
 Val Ser Glu Leu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met  
 195 200 205  
 Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser  
 210 215 220  
 Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala  
 245 250 255  
 Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val  
 260 265 270  
 Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu  
 290 295 300  
 Ile Lys Ile Gln Arg Arg Asn Ile Phe  
 305 310

<210> 91  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 91  
 atg ggc aag gaa aac tgc acc act gtg gct gag ttc att ctc ctt gga 48  
 Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 cta tca gat gtc cct gag ttg aga gtc tgc ctc ttc ctg ctg ttc ctt 96  
 Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu  
 20 25 30  
 ctc atc tat gga gtc acg ttg tta gcc aac ctg ggc atg att gca ctg 144  
 Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu  
 35 40 45  
 att cag gtc agc tct cgg ctc cac acc ccc atg tac ttt ttc ctc agc 192  
 Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 cac ttg tcc tct gta gat ttc tgc tac tcc tca ata att gtg cca aaa 240  
 His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys  
 65 70 75 80  
 atg ttg gct aat atc ttt aac aag gac aaa gcc atc tcc ttc cta ggg 288  
 Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly  
 85 90 95

104/261

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tgc atg gtg caa ttc tac ttg ttt tgc act tgt gtg gtc act gag gtc 336
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
100 105 110

ttc ctg ctg gcc gtg atg gcc tat gac cgc ttt gtg gcc atc tgt aac 384
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
115 120 125

cct ttg cta tac aca gtc acc atg tct tgg aag gtg cgt gtg gag ctg 432
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
130 135 140

gct tct tgc tgc tac ttc tgt ggg acg gtg tgt tct ctg att cat ttg 480
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
145 150 155 160

tgc tta gct ctt agg atc ccc ttc tat aga tct aat gtg att aac cac 528
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
165 170 175

ttt ttc tgt gat cta cct cct gtc tta agt ctt gct tgc tct gat atc 576
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
180 185 190

act gtg aat gag aca ctg ctg ttc ctg gtg gcc act ttg aat gag agt 624
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
195 200 205

gtt acc atc atg atc atc ctc acc tcc tac ctg cta att ctc acc acc 672
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
210 215 220

atc ctg aag atg ggc tct gca gag ggc agg cac aaa gcc ttc tcc acc 720
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
225 230 235 240

tgt gct tcc cac ctc aca gct atc act gtc ttc cat gga aca gtc ctt 768
Cys Ala Ser His Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
245 250 255

tcc att tat tgc agg ccc agt tca ggc aat agt gga gat gct gac aaa 816
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
260 265 270

gtg gcc acc gtg ttc tac aca gtc gtg att cct atg ctg aac tct gtg 864
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
275 280 285

atc tac agc ctg aga aat aaa gat gtg aaa gaa gct ctc aga aaa tgt 912
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Cys
290 295 300

gtg gtg tgg agg aag agg att atg tcc agc aaa 945
Val Val Trp Arg Lys Arg Ile Met Ser Ser Lys
305 310 315

```

&lt;210&gt; 92

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

105/261

&lt;400&gt; 92

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Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
1      5      10      15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
20      25      30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu
35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
100     105     110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
115     120     125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
130     135     140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
145     150     155     160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
165     170     175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
180     185     190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
195     200     205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
210     215     220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
225     230     235     240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
245     250     255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
260     265     270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
275     280     285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Cys
290     295     300
Val Val Trp Arg Lys Arg Ile Met Ser Ser Lys
305     310     315

```

&lt;210&gt; 93

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(945)

&lt;400&gt; 93

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atg gat caa ggg aac aag act gaa gtc acc atg ttt ata ttg aca ggc      48
Met Asp Gln Gly Asn Lys Thr Glu Val Thr Met Phe Ile Leu Thr Gly
1      5      10      15

ttc aca gat gat ttt gag ctg caa gtc ttc cta ttt tta cta ttt ttt      96
Phe Thr Asp Asp Phe Glu Leu Gln Val Phe Leu Phe Leu Leu Phe Phe
20      25      30

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106/261

gca atc tat ctc ttt acc ttg ata ggc aat tta ggg ctg gtt gtg ttg	144
Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val Leu	
35 40 45	
gtc att gag gat tcc tgg ctc cac aac ccc atg tat tat ttt ctt agt	192
Val Ile Glu Asp Ser Trp Leu His Asn Pro Met Tyr Tyr Phe Leu Ser	
50 55 60	
gtt tta tca ttc ttg gat gct tgc tat tct aca gtt gtc act cca aaa	240
Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser Thr Val Val Thr Pro Lys	
65 70 75 80	
atg ttg gtc aat ttc ctg gca aaa aat aaa tcc att tca ttt atc gga	288
Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Ile Gly	
85 90 95	
tgt gca aca cag atg ctt ctt ttt gtt act ttt gga act aca gaa tgt	336
Cys Ala Thr Gln Met Leu Leu Phe Val Thr Phe Gly Thr Thr Glu Cys	
100 105 110	
ttt ctc ttg gct gca atg gct tat gat cac tat gta gcc atc tac aac	384
Phe Leu Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Tyr Asn	
115 120 125	
cct ctc ctg tat tca gtg agc atg tca ccc aga gtc tat gtg cca ctc	432
Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro Leu	
130 135 140	
atc act gct tcc tac gtt gct ggc att tta cat gct act ata cat ata	480
Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu His Ala Thr Ile His Ile	
145 150 155 160	
gtg gct aca ttt agc ctg tcc ttc tgt gga tcc aat gaa att agg cat	528
Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg His	
165 170 175	
gtc ttt tgt gat atg cct cct ctc ctt gct att tct tgt tct gac act	576
Val Phe Cys Asp Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp Thr	
180 185 190	
cac aca aac cag ctt cta ctc ttc tac ttt gtg ggt tct att gag ata	624
His Thr Asn Gln Leu Leu Leu Phe Tyr Phe Val Gly Ser Ile Glu Ile	
195 200 205	
ata gtc act atc ctg att gtc ctg atc tcc tat ggt ttt att ctg ttg	672
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu	
210 215 220	
gcc att ctg aag atg cag tct gct gaa ggg agg aga aaa gtc ttc tct	720
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser	
225 230 235 240	
aca tgt gga gct cac cta act gga gtg aca att tat cat ggg aca atc	768
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile	
245 250 255	
ctc ttc atg tat gtg aga cca agt tcc agc tac act tcg gac aat gac	816
Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp	
260 265 270	
atg ata gtg tca ata ttt tat acc att gtg att ccc atg ctg aat ccc	864
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro	



107/261

275	280	285	
atc atc tac agt ttg cgg aac aaa gat gta aag gag gca atc aaa aga			912
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg			
290	295	300	
ttg ctt gtg aga aat tgg ttc ata aat aag tta			945
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu			
305	310	315	

<210> 94  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
 Met Asp Gln Gly Asn Lys Thr Glu Val Thr Met Phe Ile Leu Thr Gly  
 1 5 10 15  
 Phe Thr Asp Asp Phe Glu Leu Gln Val Phe Leu Phe Leu Leu Phe Phe  
 20 25 30  
 Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val Leu  
 35 40 45  
 Val Ile Glu Asp Ser Trp Leu His Asn Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser Thr Val Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Ala Thr Gln Met Leu Leu Phe Val Thr Phe Gly Thr Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Tyr Asn  
 115 120 125  
 Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro Leu  
 130 135 140  
 Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu His Ala Thr Ile His Ile  
 145 150 155 160  
 Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg His  
 165 170 175  
 Val Phe Cys Asp Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp Thr  
 180 185 190  
 His Thr Asn Gln Leu Leu Leu Phe Tyr Phe Val Gly Ser Ile Glu Ile  
 195 200 205  
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu  
 210 215 220  
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile  
 245 250 255  
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp  
 260 265 270  
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg  
 290 295 300  
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu  
 305 310 315

<210> 95  
 <211> 963  
 <212> DNA

108/261

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (963)

&lt;400&gt; 95

atg gaa tgg gaa aac caa acc att ctg gtg gaa ttt ttt ctg aag gga	48
Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly	
1 5 10 15	
cat tct gtt cac cca agg ctt gag tta ctc ttt ttt gtg cta atc ttc	96
His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe	
20 25 30	
ata atg tat gtg gtc atc ctt ctg ggg aat ggt act ctc att tta atc	144
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile	
35 40 45	
agc atc ttg gac cct cac ctt cac acc cct atg tac ttc ttt ctg ggg	192
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly	
50 55 60	
aac ctc tcc ttc ttg gac atc tgc tac acc acc acc tct att ccc tcc	240
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser	
65 70 75 80	
aca cta gtg agc ttc ctt tca gaa aga aag acc att tcc ttt tct ggc	288
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly	
85 90 95	
tgt gca gtg cag atg ttc ctt ggc ttg gcc atg ggg aca aca gag tgt	336
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys	
100 105 110	
gtg ctt ctg ggc atg atg gcc ttt gac cgc tat gtg gct atc tgc aac	384
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn	
115 120 125	
cct ctg aga tat ccc atc atc atg agc aag aat gcc tat gta ccc atg	432
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met	
130 135 140	
gct gtt ggg tcc tgg ttt gca ggg att gtc aac tct gca gta caa act	480
Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr	
145 150 155 160	
aca ttt gta gta caa ttg cct ttc tgc agg aag aat gtc atc aat cat	528
Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His	
165 170 175	
ttc tca tgt gaa att cta gct gtc atg aag ttg gcc tgt gct gac atc	576
Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile	
180 185 190	
tca ggc aat gag ttc ctc atg ctt gtg gcc aca ata ttg ttc aca ttg	624
Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu	
195 200 205	
atg cca ctg ctc ttg ata gtt atc tct tac tca tta atc att tcc agc	672
Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser	
210 215 220	

109/261

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atc ctc aag att cac tcc tct gag ggg aga agc aaa gct ttc tct acc 720
Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
225                230                235                240

tgc tca gcc cat ctg act gtg gtc ata ata ttc tat ggg acc atc ctc 768
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
                245                250                255

ttc atg tat atg aag ccc aag tct aaa gag aca ctt aat tca gat gac 816
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
                260                265                270

ttg gat gct acc gac aaa att ata tcc atg ttc tat ggg gtg atg act 864
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
                275                280                285

ccc atg atg aat cct tta atc tac agt ctt aga aac aag gat gtg aaa 912
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
                290                295                300

gag gca ttc att aag tgt ctt ctt tat gtg aag aca ctt tgt tgc tca 960
Glu Ala Phe Ile Lys Cys Leu Leu Tyr Val Lys Thr Leu Cys Cys Ser
305                310                315                320

gac
Asp
963

```

<210> 96  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

```

<400> 96
Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
1      5      10      15
His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
20      25      30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
35      40      45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
50      55      60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
65      70      75      80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly
85      90      95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
100     105     110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
115     120     125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met
130     135     140
Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr
145     150     155     160
Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His
165     170     175
Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
180     185     190
Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu
195     200     205

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110/261

Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser  
 210 215 220  
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu  
 245 250 255  
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp  
 260 265 270  
 Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr  
 275 280 285  
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 290 295 300  
 Glu Ala Phe Ile Lys Cys Leu Leu Tyr Val Lys Thr Leu Cys Cys Ser  
 305 310 315 320  
 Asp

<210> 97  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (942)

<400> 97  
 atg gac aca ggg aac tgg agc cag gta gca gaa ttc atc atc ttg ggc 48  
 Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 ttc ccc cat ctc cag ggt gtc cag att tat ctc ttc ctc ttg ttg ctt 96  
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu  
 20 25 30  
 ctc att tac ctc atg act gtg ttg gga aac ctg ctg ata ttc ctg gtg 144  
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val  
 35 40 45  
 gtc tgc ctg gac tcc cgg ctt cac aca ccc atg tac cac ttt gtc agc 192  
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 att ctc tcc ttc tca gag ctt ggc tat aca gct gcc acc atc cct aag 240  
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys  
 65 70 75 80  
 atg ctg gca aac ttg ttc agt gag aaa aag acc att tca ttc tct ggg 288  
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 tgt ctc ctg cag atc tat ttc ttt cac tcc ctt gga gcg act gag tgc 336  
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys  
 100 105 110  
 tat ctc ctg aca gct atg gcc tac gat agg tat tta gcc atc tgc cgg 384  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125

111/261

```

ccc ctc cac tac cca acc ctc atg acc cca aca ctt tgt gca gag att 432
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
    130                      135                      140

gcc att ggc tgt tgg ttg gga ggc ttg gct ggg cca gta gtt gaa att 480
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
    145                      150                      155                      160

tcc ttg att tca cgc ctc cca ttc tgt ggc ccc aat cgc att cag cac 528
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
                      165                      170                      175

gtc ttt tgt gac ttc cct cct gtg ctg agt ttg gct tgc act gat acg 576
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
                      180                      185                      190

tct aca aat gtc cta gta gat ttt gtt ata aat tcc tgc aag atc cta 624
Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
                      195                      200                      205

gcc acc ttc ctg ctg atc ctc tgc tcc tat gtg cag atc atc tgc aca 672
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
    210                      215                      220

gtg ctc aga att ccc tca gct gcc ggc aag agg aag gcc atc tcc acg 720
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
    225                      230                      235                      240

tgt gcc tcc cac ctc act gtg gtt ctc atc ttc tat ggg agc atc ctt 768
Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
                      245                      250                      255

tcc atg tat gtg cgg ctg aag aag agc tac tca ctg gac tat gac cag 816
Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
                      260                      265                      270

gcc ctg gca gtg gtc tac tca gtg ctc aca ccc ttc ctc aac ccc ttc 864
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
    275                      280                      285

atc tac agc ttg cac aac aag gag atc aag gag gct tgg aaa aag tac 912
Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
    290                      295                      300

atc tgc agg agg cag cca gcc acg gaa atg 942
Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
    305                      310

```

&lt;210&gt; 98.

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

```

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1          5          10          15
Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
    20          25          30
Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
    35          40          45

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112/261

```

Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50      55      60
Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
65      70      75      80
Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
      85      90      95
Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
      100      105      110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
      115      120      125
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
      130      135      140
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
145      150      155      160
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
      165      170      175
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
      180      185      190
Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
      195      200      205
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
      210      215      220
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
225      230      235      240
Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
      245      250      255
Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
      260      265      270
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
290      295      300
Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
305      310

```

<210> 99  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

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<400> 99
atg agt ggg gag aat gtc acc aag gtc agc acc ttc atc ctg gtg ggc   48
Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly
 1      5      10      15

ctc ccc acg gcc cca ggg ctg cag tac ctg ctc ttc ctc ctc ttc ctg   96
Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu
      20      25      30

ctc acc tac ctc ttt gtc ctg gtg gag aac ctg gcc atc atc ctc atc   144
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile
      35      40      45

gtc tgg agc agc acc tcc ctc cac agg ccc atg tac tac ttt ctg agc   192
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
      50      55      60

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113/261

tcc atg tct ttc ctg gag atc tgg tac gtg tct gac atc acc ccc aag	240
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys	
65 70 75 80	
atg ctg gag ggc ttc ctc ctc cag cag aaa cgc atc tct ttc gtc ggg	288
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly	
85 90 95	
tgc atg acg cag ctc tac ttc ttc agc tcc ctg gtg tgc acc gag tgt	336
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys	
100 105 110	
gtg ctt ctg gcc tcc atg gcc tac gac cgc tac gtg gcc atc tgc cac	384
Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His	
115 120 125	
ccg ctg cgc tac cac gtc ctt gtg acc ccg ggg ctg tgc ctc cag ctg	432
Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Leu Cys Leu Gln Leu	
130 135 140	
gtg ggc ttc tcc ttt gtg agt ggc ttc acc atc tcc atg atc aag gtc	480
Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val	
145 150 155 160	
tgt ttt atc tcc agc gtc acg ttc tgt ggc tcc aac gtc ttg aac cac	528
Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His	
165 170 175	
ttc ttc tgt gac att tcc ccc atc ctc aag ctg gcc tgc acg gac ttc	576
Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe	
180 185 190	
tcc act gca gag ctg gtg gat ttc atc ctg gcc ttc atc atc ctg gtg	624
Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val	
195 200 205	
ttt ccg ctc ctg gcc acc ata ctg tca tat tgg cac atc acc ctg gct	672
Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala	
210 215 220	
gtc ctg cgc atc ccc tcg gcc acc ggc tgc tgg aga gcc ttc tct acc	720
Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr	
225 230 235 240	
tgc gcc tct cac ctc acc gtg gtc acc gtc ttc tat aca gcc ttg ctt	768
Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu	
245 250 255	
ttc atg tat gtc cgg ccc caa gcc att gat tcc cag agc tcc aac aag	816
Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys	
260 265 270	
ctc atc tct gcc gtg tac act gtt gtc acg cca ata att aac cct ttg	864
Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu	
275 280 285	
att tac tgc ctg agg aac aag gaa ttt aag gac gcc ttg aaa aag gcc	912
Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala	
290 295 300	

114/261

ttg ggc ttg ggt cat tgg ctc cat ccc tgg  
 Leu Gly Leu Gly His Trp Leu His Pro Trp  
 305 310

942

<210> 100  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 100  
 Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly  
 1 5 10 15  
 Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Phe Leu  
 20 25 30  
 Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile  
 35 40 45  
 Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly  
 85 90 95  
 Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys  
 100 105 110  
 Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Leu Cys Leu Gln Leu  
 130 135 140  
 Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val  
 145 150 155 160  
 Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe  
 180 185 190  
 Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val  
 195 200 205  
 Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala  
 210 215 220  
 Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu  
 245 250 255  
 Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys  
 260 265 270  
 Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu  
 275 280 285  
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala  
 290 295 300  
 Leu Gly Leu Gly His Trp Leu His Pro Trp  
 305 310

<210> 101  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)



115/261

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<400> 101
atg gga agt ttc aac acc agt ttt gaa gat ggc ttc att ttg gtg gga 48
Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
1 5 10 15

ttc tca gat tgg ccg caa ctg gag ccc atc ctg ttt gtc ttt att ttt 96
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
20 25 30

att ttc tac tcc cta act ctc ttt ggc aac acc atc atc atc gct ctc 144
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
35 40 45

tcc tgg cta gac ctt cgg ctg cac aca cct atg tac ttc ttt ctc tct 192
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60

cat ctg tcc ctc ctg gac ctc tgc ttc acc acc agc acc gtg ccc cag 240
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
65 70 75 80

ctc ctg atc aac ctt tgc ggg gtg gac cgc acc atc acc cgt gga ggg 288
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
85 90 95

tgt gtg gct cag ctc ttc atc tac cta gcc ctg ggc tcc aca gag tgt 336
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
100 105 110

gtg ctc ctg gtg gtg atg gcc ttt gac cgc tat gct gct gtc tgt cgt 384
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
115 120 125

cca ctc cac tac atg gcc atc atg cac ccc cat ctc tgc cag acc ctg 432
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
130 135 140

gct atc gcc tcc tgg ggt gcg ggt ttc gtg aac tct ctg atc cag aca 480
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
145 150 155 160

ggg ctc gca atg gcc atg cct ctc tgt ggc cat cga ctg aat cac ttc 528
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
165 170 175

ttc tgt gag atg cct gta ttt ctg aag ttg gct tgt gcg gac aca gaa 576
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
180 185 190

gga aca gag gcc aag atg ttt gtg gcc cga gtc ata gtc gtg gct gtt 624
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
195 200 205

cct gca gca ctt att cta ggc tcc tat gtg cac att gct cat gca gtg 672
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
210 215 220

ctg agg gtg aag tca acg gct ggg cgc aga aag gct ttt ggg act tgt 720
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
225 230 235 240

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116/261

```

ggg tcc cac ctc cta gta gtt ttc ctt ttt tat ggc tca gcc atc tac 768
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
                245                250                255

aca tat ctc caa tcc atc cac aat tat tct gag cgt gag gga aaa ttt 816
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
                260                265                270

gtt gcc ctt ttt tat act ata att acc ccc att ctc aat cct ctc att 864
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
                275                280                285

tat aca cta aga aac aag gac gtg aag ggg gct ctg tgg aaa gta cta 912
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
                290                295                300

tgg agg ggc agg gac tca ggg cag tgg 939
Trp Arg Gly Arg Asp Ser Gly Gln Trp
305                310

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<210> 102  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

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<400> 102
Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1          5          10          15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20          25          30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ala Leu
 35          40          45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65          70          75          80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
 85          90          95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
100          105          110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
115          120          125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
130          135          140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
145          150          155          160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
165          170          175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
180          185          190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
195          200          205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
210          215          220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
225          230          235          240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
245          250          255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
260          265          270

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117/261

Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu  
 290 295 300  
 Trp Arg Gly Arg Asp Ser Gly Gln Trp  
 305 310

<210> 103  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 103  
 atg gac aca ggc aac aaa act ctg ccc cag gac ttt ctc tta ctg ggc 48  
 Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Gly  
 1 5 10 15  
 ttt cct ggt tct caa act ctt cag ctc tct ctc ttt atg ctt ttt ctg 96  
 Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu  
 20 25 30  
 gtg atg tac atc ctc aca gtt agt ggt aat gtg gct atc ttg atg ttg 144  
 Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu  
 35 40 45  
 gtg agc acc tcc cat cag ttg cat acc ccc atg tac ttc ttt ctg agc 192  
 Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 aac ctc tcc ttc ctg gag att tgg tat acc aca gca gca gtg ccc aaa 240  
 Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys  
 65 70 75 80  
 gca ctg gcc atc cta ctg ggg aga agt cag acc ata tca ttt aca agc 288  
 Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser  
 85 90 95  
 tgt ctt ttg cag atg tac ttt gtt ttc tca tta ggc tgc aca gag tac 336  
 Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr  
 100 105 110  
 ttc ctc ctg gca gcc atg gct tat gac cgc tgt ctt gcc atc tgc tat 384  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr  
 115 120 125  
 cct tta cac tac gga gcc atc atg agt agc ctg ctc tca gcg cag ctg 432  
 Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu  
 130 135 140  
 gcc ctg ggc tcc tgg gtg tgt ggt ttc gtg gcc att gca gtg ccc aca 480  
 Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr  
 145 150 155 160  
 gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc cgt gcc atc aac cac 528  
 Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His  
 165 170 175

118/261

```

ttc ttc tgt gac att gca ccc tgg att gcc ctg gcc tgc acc aac aca 576
Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr
      180      185      190

cag gca gta gag ctt gtg gcc ttt gtg att gct gtt gtg gtt atc ctg 624
Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Val Ile Leu
      195      200      205

agt tca tgc ctc atc acc ttt gtc tcc tat gtg tac atc atc agc acc 672
Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr
      210      215      220

atc ctc agg atc ccc tct gcc ata gaa ggc aag agg aag gcc ttc tca 720
Ile Leu Arg Ile Pro Ser Ala Ile Glu Gly Lys Arg Lys Ala Phe Ser
      225      230      235      240

aca tgc tca tct cat ctc aca gtg gtg acc ctt tac tat tct cct gta 768
Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val
      245      250      255

atc tac acc tat atc cgc cct gct tcc agc tat aca ttt gaa aga gac 816
Ile Tyr Thr Tyr Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp
      260      265      270

aag gtg gta gct gca ctc tat act ctt gtg act ccc aca tta aac ccg 864
Lys Val Val Ala Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro
      275      280      285

atg gtg tac agc ttc cag aat agg gag atg cag gca gga att agg aag 912
Met Val Tyr Ser Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys
      290      295      300

ctt ctg cac agc aaa aga aac tat cat cag agt 945
Leu Leu His Ser Lys Arg Asn Tyr His Gln Ser
      305      310      315

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&lt;210&gt; 104

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly
1      5      10      15
Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu
      20      25      30
Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu
      35      40      45
Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys
      65      70      75      80
Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser
      85      90      95
Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr
      100      105      110
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr
      115      120      125
Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu
      130      135      140

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119/261

Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr  
 145 150 155 160  
 Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr  
 180 185 190  
 Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Ile Leu  
 195 200 205  
 Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ala Ile Glu Gly Lys Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val  
 245 250 255  
 Ile Tyr Thr Tyr Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp  
 260 265 270  
 Lys Val Val Ala Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro  
 275 280 285  
 Met Val Tyr Ser Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys  
 290 295 300  
 Leu Leu His Ser Lys Arg Asn Tyr His Gln Ser  
 305 310 315

&lt;210&gt; 105

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(945)

&lt;400&gt; 105

atg act ggg gga gga aat att aca gaa atc acc tat ttc atc ctg ctg 48  
 Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu  
 1 5 10 15  
 gga ttc tca gat ttt ccc agg atc ata aaa gtg ctc ttc act ata ttc 96  
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe  
 20 25 30  
 ctg gtg atc tac att aca tct ctg gcc tgg aac ctc tcc ctc att gtt 144  
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val  
 35 40 45  
 tta ata agg atg gat tcc cac ctc cat aca ccc atg tat ttc ttc ctc 192  
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 agt aac ctg tcc ttc ata gat gtc tgc tat atc agc tcc aca gtc ccc 240  
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro  
 65 70 75 80  
 aag atg ctc tcc aac ctc tta cag gaa cag caa act atc act ttt gtt 288  
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val  
 85 90 95  
 ggt tgt att att cag tac ttt atc ttt tca acg atg gga ctg agt gag 336  
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu  
 100 105 110

120/261

tct tgt ctc atg aca gcc atg gct tat gat cgt tat gct gcc att tgt	384
Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys	
115 120 125	
aac ccc ctg ctc tat tca tcc atc atg tca ccc acc ctc tgt gtt tgg	432
Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp	
130 135 140	
atg gta ctg gga gcc tac atg act ggc ctc act gct tct tta ttc caa	480
Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln	
145 150 155 160	
att ggt gct ttg ctt caa ctc cac ttc tgt ggg tct aat gtc atc aga	528
Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg	
165 170 175	
cat ttc ttc tgt gac atg ccc caa ctg tta atc ttg tcc tgt act gac	576
His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp	
180 185 190	
act ttc ttt gta cag gtc atg act gct ata tta acc atg ttc ttt ggg	624
Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly	
195 200 205	
ata gca agt gcc cta gtt atc atg ata tcc tat ggc tat att ggc atc	672
Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile	
210 215 220	
tcc atc atg aag atc act tca gct aaa ggc agg tcc aag gca ttc aac	720
Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Ser Lys Ala Phe Asn	
225 230 235 240	
acc tgt gct tct cat cta aca gct gtt tcc ctc ttc tat aca tca gga	768
Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly	
245 250 255	
atc ttt gtc tat ttg agt tcc agc tct gga ggt tct tca agc ttt gac	816
Ile Phe Val Tyr Leu Ser Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp	
260 265 270	
aga ttt gca tct gtt ttc tac act gtg gtc att ccc atg tta aat ccc	864
Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro	
275 280 285	
ttg att tac agt ttg agg aac aaa gaa att aaa gat gcc tta aag agg	912
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg	
290 295 300	
ttg caa aag aga aac tgg gga agc tca aac tgg	945
Leu Gln Lys Arg Asn Trp Gly Ser Ser Asn Trp	
305 310 315	

&lt;210&gt; 106

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu

1

5

10

15

121/261

Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe  
 20 25 30  
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val  
 35 40 45  
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro  
 65 70 75 80  
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Thr Ile Thr Phe Val  
 85 90 95  
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu  
 100 105 110  
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp  
 130 135 140  
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln  
 145 150 155 160  
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg  
 165 170 175  
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp  
 180 185 190  
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly  
 195 200 205  
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile  
 210 215 220  
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Ser Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly  
 245 250 255  
 Ile Phe Val Tyr Leu Ser Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp  
 260 265 270  
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg  
 290 295 300  
 Leu Gln Lys Arg Asn Trp Gly Ser Ser Asn Trp  
 305 310 315

<210> 107  
 <211> 936  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(936)

<400> 107  
 atg aaa aaa gaa caa gat tct aat gtg aca gaa ttt gtt ctt ctg ggc 48  
 Met Lys Lys Glu Gln Asp Ser Asn Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 cta tca tct tct tgg gag ctg cag cta ttt ctc ttc tta cta ttt ttg 96  
 Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Phe Leu Leu Phe Leu  
 20 25 30  
 ttt ttt tac att gct att gtc ctg gga aac ctc ttg ata gtg gta aca 144  
 Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val Val Thr  
 35 40 45

122/261

gtg	caa	gcc	cat	gct	cac	ctg	ctc	caa	tct	cct	atg	tat	tat	ttt	tta	192
Val	Gln	Ala	His	Ala	His	Leu	Leu	Gln	Ser	Pro	Met	Tyr	Tyr	Phe	Leu	
	50					55				60						
ggt	cat	ctc	tct	ttc	att	gac	cta	tgc	ctg	agc	tgt	gtt	act	gtg	cca	240
Gly	His	Leu	Ser	Phe	Ile	Asp	Leu	Cys	Leu	Ser	Cys	Val	Thr	Val	Pro	
	65				70					75					80	
aag	atg	tta	ggg	gat	ttc	cta	cag	cag	ggc	aag	agc	atc	tct	ttt	tca	288
Lys	Met	Leu	Gly	Asp	Phe	Leu	Gln	Gln	Gly	Lys	Ser	Ile	Ser	Phe	Ser	
				85					90					95		
gga	tgc	ctg	gcc	cag	atc	tac	ttc	ctc	cac	ttt	cta	gga	gcc	agt	gag	336
Gly	Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Leu	His	Phe	Leu	Gly	Ala	Ser	Glu	
			100					105					110			
atg	ttt	ttg	ctg	aca	gtc	atg	gcc	tat	gac	agg	tat	gtt	gcc	atc	tgt	384
Met	Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	
		115					120					125				
aac	cct	ttg	cgc	tac	ctt	aca	gtc	atg	aac	ccc	cag	cta	tgc	ctt	tgg	432
Asn	Pro	Leu	Arg	Tyr	Leu	Thr	Val	Met	Asn	Pro	Gln	Leu	Cys	Leu	Trp	
	130					135					140					
ttg	gtt	ctt	gcc	tgc	tgg	tgt	ggg	ggt	ttt	atc	cac	tct	atc	atg	cag	480
Leu	Val	Leu	Ala	Cys	Trp	Cys	Gly	Gly	Phe	Ile	His	Ser	Ile	Met	Gln	
	145				150				155						160	
acc	ctc	ctg	acc	ttc	cag	ctg	ccc	ttc	tgt	aat	gct	cag	gtt	ata	gac	528
Thr	Leu	Leu	Thr	Phe	Gln	Leu	Pro	Phe	Cys	Asn	Ala	Gln	Val	Ile	Asp	
				165					170					175		
cat	tac	ttt	tgt	gat	gtc	cac	cca	gtc	cta	aaa	ctt	gcc	tgt	gct	gat	576
His	Tyr	Phe	Cys	Asp	Val	His	Pro	Val	Leu	Lys	Leu	Ala	Cys	Ala	Asp	
			180					185					190			
aca	act	ctg	ata	aat	atg	ttg	gta	gtt	gcc	aac	agt	ggt	ctc	atc	tcc	624
Thr	Thr	Leu	Ile	Asn	Met	Leu	Val	Val	Ala	Asn	Ser	Gly	Leu	Ile	Ser	
		195				200						205				
ctg	ggt	tgt	ttc	ctc	att	ctt	ttg	gcc	tcc	tac	aaa	gtc	att	ctg	ctt	672
Leu	Gly	Cys	Phe	Leu	Ile	Leu	Leu	Ala	Ser	Tyr	Lys	Val	Ile	Leu	Leu	
	210					215					220					
agt	ctt	caa	aaa	cag	tct	gca	gag	agc	cga	cgc	aaa	gct	ctc	tct	acc	720
Ser	Leu	Gln	Lys	Gln	Ser	Ala	Glu	Ser	Arg	Arg	Lys	Ala	Leu	Ser	Thr	
	225				230					235					240	
tgt	gga	tct	cat	ctg	act	gta	gta	act	ttc	ttc	ttt	gtt	ccg	tgt	atc	768
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Thr	Phe	Phe	Phe	Val	Pro	Cys	Ile	
				245					250					255		
ttt	att	tat	ctc	cgt	cca	tcc	act	act	ttc	cca	ttg	gat	aaa	gct	gtg	816
Phe	Ile	Tyr	Leu	Arg	Pro	Ser	Thr	Thr	Phe	Pro	Leu	Asp	Lys	Ala	Val	
			260					265					270			
tct	gtg	ttc	tat	acc	acc	atc	acc	cca	atg	ttg	aac	cca	ctc	atc	tat	864
Ser	Val	Phe	Tyr	Thr	Thr	Ile	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	
		275					280					285				



123/261

act ctg agg aat gag gat gta aag aat gcc atg agg cag cta tgg agt 912  
 Thr Leu Arg Asn Glu Asp Val Lys Asn Ala Met Arg Gln Leu Trp Ser  
 290 295 300

agc aag atc tcc ttg aag gaa aaa 936  
 Ser Lys Ile Ser Leu Lys Glu Lys  
 305 310

<210> 108  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 108  
 Met Lys Lys Glu Gln Asp Ser Asn Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val Val Thr  
 35 40 45  
 Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr Phe Leu  
 50 55 60  
 Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr Val Pro  
 65 70 75 80  
 Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser Phe Ser  
 85 90 95  
 Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala Ser Glu  
 100 105 110  
 Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln Leu Cys Leu Trp  
 130 135 140  
 Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile Met Gln  
 145 150 155 160  
 Thr Leu Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp  
 165 170 175  
 His Tyr Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp  
 180 185 190  
 Thr Thr Leu Ile Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser  
 195 200 205  
 Leu Gly Cys Phe Leu Ile Leu Leu Ala Ser Tyr Lys Val Ile Leu Leu  
 210 215 220  
 Ser Leu Gln Lys Gln Ser Ala Glu Ser Arg Arg Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Thr Phe Phe Phe Val Pro Cys Ile  
 245 250 255  
 Phe Ile Tyr Leu Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val  
 260 265 270  
 Ser Val Phe Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Glu Asp Val Lys Asn Ala Met Arg Gln Leu Trp Ser  
 290 295 300  
 Ser Lys Ile Ser Leu Lys Glu Lys  
 305 310

<210> 109  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

124/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(942)

&lt;400&gt; 109

atg	aaa	ggg	gca	aac	ctg	agc	caa	ggg	atg	gag	ttt	gag	ctc	ttg	ggc	48
Met	Lys	Gly	Ala	Asn	Leu	Ser	Gln	Gly	Met	Glu	Phe	Glu	Leu	Leu	Gly	
1				5					10					15		
ctc	acc	act	gac	ccc	cag	ctc	cag	agg	ctg	ctc	ttc	gtg	gtg	ttc	ctg	96
Leu	Thr	Thr	Asp	Pro	Gln	Leu	Gln	Arg	Leu	Leu	Phe	Val	Val	Phe	Leu	
			20					25					30			
ggc	atg	tac	aca	gcc	act	ctg	ctg	ggg	aac	ctg	gtc	atg	ttc	ctc	ctg	144
Gly	Met	Tyr	Thr	Ala	Thr	Leu	Leu	Gly	Asn	Leu	Val	Met	Phe	Leu	Leu	
		35					40					45				
atc	cat	gtg	agt	gcc	acc	ctg	cac	aca	ccc	atg	tac	tcc	ctc	ctg	aag	192
Ile	His	Val	Ser	Ala	Thr	Leu	His	Thr	Pro	Met	Tyr	Ser	Leu	Leu	Lys	
	50					55					60					
agc	ctc	tcc	ttc	ttg	gat	ttc	tgc	tac	tcc	tcc	acg	gtt	gtg	ccc	cag	240
Ser	Leu	Ser	Phe	Leu	Asp	Phe	Cys	Tyr	Ser	Ser	Thr	Val	Val	Pro	Gln	
65					70					75					80	
acc	ctg	gtg	aac	ttc	ttg	gcc	aag	agg	aaa	gtg	atc	tct	tat	ttt	ggc	288
Thr	Leu	Val	Asn	Phe	Leu	Ala	Lys	Arg	Lys	Val	Ile	Ser	Tyr	Phe	Gly	
			85						90					95		
tgc	atg	act	cag	atg	ttc	ttc	tat	gcg	ggt	ttt	gcc	acc	agt	gag	tgc	336
Cys	Met	Thr	Gln	Met	Phe	Phe	Tyr	Ala	Gly	Phe	Ala	Thr	Ser	Glu	Cys	
			100					105					110			
tat	ctc	atc	gct	gcc	atg	gcc	tat	gac	cgc	tat	gcc	gct	att	tgt	aac	384
Tyr	Leu	Ile	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	Asn	
		115					120					125				
ccc	ctg	ctc	tac	tca	acc	atc	atg	tct	cct	gag	gtc	tgt	gcc	tcg	ctg	432
Pro	Leu	Leu	Tyr	Ser	Thr	Ile	Met	Ser	Pro	Glu	Val	Cys	Ala	Ser	Leu	
	130					135					140					
att	gtg	ggc	tcc	tac	agt	gca	gga	ttc	ctc	aat	tct	ctt	atc	cac	act	480
Ile	Val	Gly	Ser	Tyr	Ser	Ala	Gly	Phe	Leu	Asn	Ser	Leu	Ile	His	Thr	
145					150					155				160		
ggc	tgt	atc	ttt	agt	ctg	aaa	ttc	tgc	ggt	gct	cat	gtc	gtc	act	cac	528
Gly	Cys	Ile	Phe	Ser	Leu	Lys	Phe	Cys	Gly	Ala	His	Val	Val	Thr	His	
				165				170					175			
ttc	ttc	tgt	gat	ggg	cca	ccc	atc	ctg	tcc	ttg	tct	tgt	gta	gac	acc	576
Phe	Phe	Cys	Asp	Gly	Pro	Pro	Ile	Leu	Ser	Leu	Ser	Cys	Val	Asp	Thr	
			180					185					190			
tca	ctg	tgt	gag	atc	ctg	ctc	ttc	att	ttt	gct	ggg	ttc	aac	ctt	ttg	624
Ser	Leu	Cys	Glu	Ile	Leu	Leu	Phe	Ile	Phe	Ala	Gly	Phe	Asn	Leu	Leu	
		195					200					205				
agc	tgc	acc	ctc	acc	atc	ttg	atc	tcc	tac	ttc	tta	att	ctc	aac	acc	672
Ser	Cys	Thr	Leu	Thr	Ile	Leu	Ile	Ser	Tyr	Phe	Leu	Ile	Leu	Asn	Thr	
	210					215					220					

125/261

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atc ctg aaa atg agc tcg gcc cag ggc agg ttt aag gca ttt tcc acc 720
Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
225                230                235                240

tgt gca tcc cac ctc act gcc atc tgc ctc ttc ttt ggc aca aca ctt 768
Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu
                245                250                255

ttt atg tac ctg cgc ccc agg tcc agc tac tcc ttg acc cag gac cgc 816
Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg
                260                265                270

aca gtt gct gtc atc tac aca gtg gtg atc cca gtg ctg aac ccc ctc 864
Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
                275                280                285

atg tac tct ttg aga aac aag gat gtg aag aaa gct tta ata aag tta 912
Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu
                290                295                300

ctt acc tgt atg ttt tcc ccc aca aga tgg 942
Leu Thr Cys Met Phe Ser Pro Thr Arg Trp
305                310

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<210> 110  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 110
Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1          5          10          15
Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
          20          25          30
Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu
          35          40          45
Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys
          50          55          60
Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln
          65          70          75          80
Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly
          85          90          95
Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys
          100          105          110
Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu
          130          135          140
Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr
          145          150          155          160
Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His
          165          170          175
Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr
          180          185          190
Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu
          195          200          205
Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr
          210          215          220
Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
          225          230          235          240

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[illegible]

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<220>
<221> CDS
<222> (1) ... (942)
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INSTRUCID: CWO 03000735A2 | 5

127/261

cta gtt att ttc cac ctc tca ttc tgc agc tcc cat gaa atc cag cac 528  
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His  
                     165                    170                    175

ttt ttt tgt gac acg cca cct gtg ctg agc cta gcc tgt gga gat aca 576  
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr  
                     180                    185                    190

ggc ccg agt gag ctg agg atc ttt atc ctc agt ctt ttg gtc ctc ttg 624  
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu  
                     195                    200                    205

gtc tcc ttc ttc ttc atc acc atc tcc tac gcc tac atc ttg gca gca 672  
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala  
                     210                    215                    220

ata ctg agg atc ccc tct gct gag ggg cag aag aag gcc ttc tcc act 720  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr  
                     225                    230                    235                    240

tgt gcc tcg cac ctt aca gtg gtc att att cat tat gcc tgt gct tcc 768  
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
                     245                    250                    255

ttc gtg tac ctg agg ccc aaa gcc agc tac tct ctt gag aga gat cag 816  
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln  
                     260                    265                    270

ctt att gcc atg acc tat act gta gtg acc ccc ctc ctt aat ccc att 864  
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile  
                     275                    280                    285

gtt tat agt cta agg act agg gct ata cag aca gct ctg agg aat gct 912  
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala  
                     290                    295                    300

ttc aga ggg aga ttg ctg ggg agc cag tgg 942  
 Phe Arg Gly Arg Leu Leu Gly Ser Gln Trp  
                     305                    310

&lt;210&gt; 112

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly  
 1                    5                    10                    15  
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu  
                     20                    25                    30  
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala  
                     35                    40                    45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
                     50                    55                    60  
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg  
                     65                    70                    75                    80  
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly  
                     85                    90                    95  
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys  
                     100                    105                    110

128/261

Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala  
 115 120 125  
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu  
 130 135 140  
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr  
 145 150 155 160  
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His  
 165 170 175  
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu  
 195 200 205  
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
 245 250 255  
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln  
 260 265 270  
 Leu Ile Ala Met Thr Tyr Thr Val Thr Pro Leu Leu Asn Pro Ile  
 275 280 285  
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala  
 290 295 300  
 Phe Arg Gly Arg Leu Leu Gly Ser Gln Trp  
 305 310

<210> 113  
 <211> 933  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(933)

<400> 113  
 aaa aat cag act gct gga gtc acc ttc atc ctc ttg ggc ttc tca gaa 48  
 Lys Asn Gln Thr Ala Gly Val Thr Phe Ile Leu Leu Gly Phe Ser Glu  
 1 5 10 15  
 ttt cca gac ctt cag ata ccc ctg ttc ctg gtc ttc ctg acc atc tac 96  
 Phe Pro Asp Leu Gln Ile Pro Leu Phe Leu Val Phe Leu Thr Ile Tyr  
 20 25 30  
 aca atc act gtg atg ggg aat ctg ggc atg atc atg gtc atc agg atc 144  
 Thr Ile Thr Val Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile  
 35 40 45  
 aac ccc aaa ctc cac acc cct atg tac ttt ttc ctc agc cac ttg tcc 192  
 Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser  
 50 55 60  
 ttt gtt gat ttc tgt tat tcc acc aca att aca cca aaa ctg ctg gag 240  
 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu  
 65 70 75 80  
 aac ttg gtt gtg gaa gac aga atc atc tcc ttc aca gga tgc atc atg 288  
 Asn Leu Val Val Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met  
 85 90 95

129/261

caa ttc ttc ttt gcc tgt ata ttt gtg gtg aca gaa aca ttc atg ctg	336
Gln Phe Phe Phe Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu	
100 105 110	
gca gcg atg gct tat gac aga ttt gtg gca gtg tgt aac cct ctg ctt	384
Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu	
115 120 125	
tac aca gtt gca atg tcc cag agg ctt tgc tcc ttg tta gtg gct gca	432
Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala	
130 135 140	
tca tac tct tgg agt tta gtt tgt tcc tta aca tac aca tac ttt ctg	480
Ser Tyr Ser Trp Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu	
145 150 155 160	
ttg act tta tct ttt tgt agg act aac ttc att aat aac ttt gtc tgt	528
Leu Thr Leu Ser Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys	
165 170 175	
gag cac gct gcc att gtt gct gtg tcc tgc tct gac ccc tac atg agc	576
Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser	
180 185 190	
cag aag gtc att tta gtt tct gca aca ttc aat gaa ata agc agc gtg	624
Gln Lys Val Ile Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Val	
195 200 205	
gtg atc att ctc act tcc tat gct ttc att ttt atc act gtc atg aag	672
Val Ile Ile Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys	
210 215 220	
atg cct tcc act ggg ggg cgc aag aaa gcg ttc tcc acg tgt gcc tcc	720
Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser	
225 230 235 240	
cac ctg acc gcc att acc att ttc cat ggg act atc ctt ttt ctc tac	768
His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr	
245 250 255	
tgt gtt cct aac tcc aaa agt tca tgg ctc atg gtc aag gtg gcc tct	816
Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser	
260 265 270	
gtc ttt tac aca gtg gtc att ccc atg ctg aac ccc ttg atc tat agc	864
Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser	
275 280 285	
ctc agg aac aaa gat gta aaa gag aca gtc agg aag tta gtc att acc	912
Leu Arg Asn Lys Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr	
290 295 300	
aaa tta tta tgt cat aaa atg	933
Lys Leu Leu Cys His Lys Met	
305 310	

&lt;210&gt; 114

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

130/261

<400> 114  
 Lys Asn Gln Thr Ala Gly Val Thr Phe Ile Leu Leu Gly Phe Ser Glu  
 1 5 10 15  
 Phe Pro Asp Leu Gln Ile Pro Leu Phe Leu Val Phe Leu Thr Ile Tyr  
 20 25 30  
 Thr Ile Thr Val Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile  
 35 40 45  
 Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser  
 50 55 60  
 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu  
 65 70 75 80  
 Asn Leu Val Val Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met  
 85 90 95  
 Gln Phe Phe Phe Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu  
 100 105 110  
 Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu  
 115 120 125  
 Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala  
 130 135 140  
 Ser Tyr Ser Trp Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu  
 145 150 155 160  
 Leu Thr Leu Ser Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys  
 165 170 175  
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser  
 180 185 190  
 Gln Lys Val Ile Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Val  
 195 200 205  
 Val Ile Ile Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys  
 210 215 220  
 Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser  
 225 230 235 240  
 His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr  
 245 250 255  
 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser  
 260 265 270  
 Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Lys Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr  
 290 295 300  
 Lys Leu Leu Cys His Lys Met  
 305 310

<210> 115  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(957)

<400> 115  
 atg caa cca tat acc aaa aac tgg acc cag gta act gaa ttt gtc atg 48  
 Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met  
 1 5 10 15  
 atg ggc ttt gct ggc atc cat gaa gca cac ctc ctc ttc ttc ata ctc 96  
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu  
 20 25 30



131/261

ttc ctc acc atg tac ctg ttc acc ttg gtg gag aat ttg gcc atc att	144
Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile	
35 40 45	
tta gtg gtg ggt ttg gac cac cga cta cgg aga ccc atg tat ttc ttc	192
Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe	
50 55 60	
ctg aca cac ttg tcc tgc ctt gaa atc tgg tac act tct gtt aca gtg	240
Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val	
65 70 75 80	
ccc aag atg ctg gct ggt ttt att ggg gtg gat ggt ggc aag aat atc	288
Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile	
85 90 95	
tct tat gct ggt tgc cta tcc cag ctc ttc atc ttc acc ttt ctt ggg	336
Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly	
100 105 110	
gca act gag tgt ttc cta ctg gct gcc atg gcc tat gat cgt tat gtg	384
Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val	
115 120 125	
gcc att tgt atg cct ctc cac tat ggg gct ttt gtg tcc tgg ggc acc	432
Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr	
130 135 140	
tgc atc cgt ctg gca gct gcc tgt tgg ctg gta ggt ttc ctc aca ccc	480
Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro	
145 150 155 160	
atc ttg cca atc tac ctc ttg tct cag cta aca ttt tgt ggc cca aat	528
Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn	
165 170 175	
gtc att gac cat ttc tcc tgt gat gcc tca ccc ttg cta gcc ttg tgc	576
Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser	
180 185 190	
tgc tca gat gtc act tgg aag gag act gtg gat ttc ctg gtg tct ctg	624
Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu	
195 200 205	
gct gtg cta ctg gcc tcc tct atg gtc att gct gtg tcc tat ggc aac	672
Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn	
210 215 220	
atc gtc tgg aca ctg ctg cac atc cgc tca gct gct gag cgc tgg aag	720
Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys	
225 230 235 240	
gcc ttc tct acc tgt gca gct cac ctg act gtg gtg agc ctc ttc tat	768
Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr	
245 250 255	
ggc act ctt ttc ttt atg tat gtc cag acc aag gtg acc tcc tcc atc	816
Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile	
260 265 270	

132/261

aac ttc aac aag gtg gta tct gtc ttc tac tct gtt gtc acg ccc atg 864  
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met  
 275 280 285  
 ctc aat cct ctc atc tac agt ctt agg aac aag gaa gtg aag gga gct 912  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala  
 290 295 300  
 ctg ggt cga aca ctt ctc aaa aga aga cat tta tgc agc caa aaa 957  
 Leu Gly Arg Thr Leu Leu Lys Arg Arg His Leu Cys Ser Gln Lys  
 305 310 315

&lt;210&gt; 116

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met  
 1 5 10 15  
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu  
 20 25 30  
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile  
 35 40 45  
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val  
 65 70 75 80  
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile  
 85 90 95  
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly  
 100 105 110  
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr  
 130 135 140  
 Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro  
 145 150 155 160  
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn  
 165 170 175  
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser  
 180 185 190  
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu  
 195 200 205  
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn  
 210 215 220  
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile  
 260 265 270  
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met  
 275 280 285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala  
 290 295 300  
 Leu Gly Arg Thr Leu Leu Lys Arg Arg His Leu Cys Ser Gln Lys  
 305 310 315

133/261

<210> 117  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 117  
 atg aaa aac aga acc atg ttt ggt gag ttt att cta ctg ggc ctt aca 48  
 Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 aat caa cct gaa ctc caa gtg atg ata ttc atc ttt ctg ttc ctc acc 96  
 Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr  
 20 25 30  
 tac atg cta agt atc cta gga aat ctg act att atc acc ctc acc tta 144  
 Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu  
 35 40 45  
 cta gac ccc cac ctc cag acc ccc atg tat ttc ttc ctc cgg aat ttc 192  
 Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe  
 50 55 60  
 tcc ttc tta gaa att tcc ttc aca tcc att ttt att ccc aga ttt ctg 240  
 Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu  
 65 70 75 80  
 acc agc atg aca aca gga aat aaa gtt atc agc ttt gct ggc tgc ttg 288  
 Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu  
 85 90 95  
 act cag tat ttt ttt gct ata ttt ctt gga gct acc gag ttt tac ctc 336  
 Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu  
 100 105 110  
 ctg gcc tcc atg tct tat gat cgt tat gtg gcc atc tgc aaa ccc ttg 384  
 Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 cat tac ctg act att atg agc agc aga gtc tgc ata caa cta gtg ttc 432  
 His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe  
 130 135 140  
 tgc tcc tgg ttg ggg gga ttc cta gca atc tta cca cca atc atc ctg 480  
 Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu  
 145 150 155 160  
 atg acc cag gta gat ttc tgt gtc tcc aac att ctg aat cac tat tac 528  
 Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr  
 165 170 175  
 tgt gac tat ggg cct ctc gtg gag ctt gcc tgc tca gac aca agc ctc 576  
 Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu  
 180 185 190  
 tta gaa ctg atg atc tcc gtg atg aca gcc acc ata gtc ttc att atg 624  
 Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met  
 195 200 205

134/261

atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt gcc 672  
 Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala  
 210 215 220  
 atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc acc 720  
 Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr  
 225 230 235 240  
 tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc agc 768  
 Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser  
 245 250 255  
 atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac cgc 816  
 Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg  
 260 265 270  
 gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc atc 864  
 Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile  
 275 280 285  
 atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac ttg 912  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu  
 290 295 300  
 gtg gaa gga aaa cac tcc cat ccc tct gtg 942  
 Val Glu Gly Lys His Ser His Pro Ser Val  
 305 310

&lt;210&gt; 118

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr  
 20 25 30  
 Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu  
 35 40 45  
 Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe  
 50 55 60  
 Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu  
 65 70 75 80  
 Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu  
 85 90 95  
 Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu  
 100 105 110  
 Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe  
 130 135 140  
 Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu  
 145 150 155 160  
 Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr  
 165 170 175  
 Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu  
 180 185 190  
 Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met  
 195 200 205

135/261

Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala  
 210 215 220  
 Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser  
 245 250 255  
 Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg  
 260 265 270  
 Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu  
 290 295 300  
 Val Glu Gly Lys His Ser His Pro Ser Val  
 305 310

<210> 119  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 119  
 atg aca cta gga aac agc act gaa gtc act gaa ttc tat ctt ctg gga 48  
 Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly  
 1 5 10 15  
 ttt ggt gcc cag cat gag ttt tgg tgt atc ctc ttc att gta ttc ctt 96  
 Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu  
 20 25 30  
 ctc atc tat gtg acc tcc ata atg ggt aat agt gga ata atc tta ctc 144  
 Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu  
 35 40 45  
 atc aac aca gat tcc aga ttt caa aca ctc acg tac ttt ttt cta caa 192  
 Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln  
 50 55 60  
 cat ttg gct ttt gtt gat atc tgt tac act tct gct atc act ccc aag 240  
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys  
 65 70 75 80  
 atg ctc caa agc ttc aca gaa gaa aag aat ttg ata tta ttt cag ggc 288  
 Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Ile Leu Phe Gln Gly  
 85 90 95  
 tgt gtg ata caa ttc tta gtt tat gca aca ttt gca acc agt gac tgt 336  
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys  
 100 105 110  
 tat ctc ctg gct atg atg gca gtg gat cct tat gtt gcc atc tgt aag 384  
 Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys  
 115 120 125  
 ccc ctt cac tat act gta atc atg tcc cga aca gtc tgc atc cgt ttg 432  
 Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu  
 130 135 140

136/261

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gta gct ggt tca tac atc atg ggc tca ata aat gcc tct gta caa aca 480
Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr
145                               150                               155                               160

ggt ttt aca tgt tca ctg tcc ttc tgc aag tcc aat agc atc aat cac 528
Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
165                               170                               175

ttt ttc tgt gat gtt ccc cct att ctt gct ctt tca tgc tcc aat gtt 576
Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
180                               185                               190

gac atc aac atc atg cta ctt gtt gtc ttt gtg gga tct aac ttg ata 624
Asp Ile Asn Ile Met Leu Leu Val Phe Val Gly Ser Asn Leu Ile
195                               200                               205

ttc act ggg ttg gtc gtc atc ttt tcc tac atc tac atc atg gcc acc 672
Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
210                               215                               220

atc ctg aaa atg tct tct agt gca gga agg aaa aaa tcc ttc tca aca 720
Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
225                               230                               235                               240

tgt gct tcc cac ctg acc gca gtc acc att ttc tat ggg aca ctc tct 768
Cys Ala Ser His Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
245                               250                               255

tac atg tat ttg cag tct cat tct aat aat tcc cag gaa aat atg aaa 816
Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
260                               265                               270

gtg gcc ttt ata ttt tat ggc aca gtt att ccc atg tta aat cct tta 864
Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
275                               280                               285

atc tat agc ttg aga aat aag gaa gta aaa gaa gct tta aaa aca ctt 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Thr Leu
290                               295                               300

ctc aaa aga aga cat tta tgc agc caa caa 942
Leu Lys Arg Arg His Leu Cys Ser Gln Gln
305                               310

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<210> 120  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 120
Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly
1      5      10
Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu
20      25      30
Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu
35      40      45
Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln
50      55      60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
65      70      75      80

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137/261

Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Ile Leu Phe Gln Gly  
85 90 95  
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys  
100 105 110  
Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys  
115 120 125  
Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu  
130 135 140  
Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr  
145 150 155 160  
Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His  
165 170 175  
Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val  
180 185 190  
Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile  
195 200 205  
Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr  
210 215 220  
Ile Leu Lys Met Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr  
225 230 235 240  
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser  
245 250 255  
Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys  
260 265 270  
Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu  
275 280 285  
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Thr Leu  
290 295 300  
Leu Lys Arg Arg His Leu Cys Ser Gln Gln  
305 310

<210> 121  
<211> 951  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(951)

<400> 121  
atg gct ggg gaa aac cat act aca ctg cct gaa ttc ctc ctt ctg gga 48  
Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly  
1 5 10 15  
ttc tct gac ctc aag gcc ctg cag ggc ccc ctg ttc tgg gtg gtg ctt 96  
Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu  
20 25 30  
ctg gtc tac ctg gtc acc ttg ctg ggt aac tcc ctg atc atc ctc ctc 144  
Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu  
35 40 45  
aca cag gtc agc cct gcc ctg cac tcc ccc atg tac ttc ttc ctg cgc 192  
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg  
50 55 60  
caa ctc tca gtg gtg gag ctc ttc tac acc act gac atc gtg ccc agg 240  
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg  
65 70 75 80

138/261

acc ctg gcc aat ctg ggc tcc ccg cat ccc cag gcc atc tct ttc cag	288
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln	
85 90 95	
ggc tgt gca gcc cag atg tac gtc ttc att gtc ctg gcc atc tcg gag	336
Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu	
100 105 110	
tgc tgc ctg ctc acg gcc atg gcc tat gac cga tat gtt gcc atc tgc	384
Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys	
115 120 125	
cag ccc cta cgc tat tcc acc ctc ttg agc cca cgg gcc tgc atg gcc	432
Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala	
130 135 140	
atg gtg ggt acc tcc tgg ctc aca ggc atc atc acg gcc acc acc cat	480
Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His	
145 150 155 160	
gcc tcc ctc atc ttc tct cta cct ttt cgc agc cac ccg atc atc ccg	528
Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro	
165 170 175	
cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg gca agt gct ggg	576
His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly	
180 185 190	
aag cac agg agc gag atc tcc gtg atg aca gcc acc ata gtc ttc att	624
Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile	
195 200 205	
atg atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt	672
Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly	
210 215 220	
gcc atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc	720
Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser	
225 230 235 240	
acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc	768
Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala	
245 250 255	
agc atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac	816
Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp	
260 265 270	
cgc gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc	864
Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro	
275 280 285	
atc atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac	912
Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His	
290 295 300	
ttg agg tta ata aga aaa aaa aaa aaa tcc tca caa att	951
Leu Arg Leu Ile Arg Lys Lys Lys Lys Ser Ser Gln Ile	
305 310 315	

&lt;210&gt; 122



139/261

<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 122  
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu  
 20 25 30  
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu  
 35 40 45  
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg  
 65 70 75 80  
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln  
 85 90 95  
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu  
 100 105 110  
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala  
 130 135 140  
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His  
 145 150 155 160  
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro  
 165 170 175  
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly  
 180 185 190  
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile  
 195 200 205  
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly  
 210 215 220  
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala  
 245 250 255  
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp  
 260 265 270  
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro  
 275 280 285  
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His  
 290 295 300  
 Leu Arg Leu Ile Arg Lys Lys Lys Lys Ser Ser Gln Ile  
 305 310 315

<210> 123  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(951)

<400> 123  
 atg gga aag acc aaa aac aca tcg ctg gat gcc gtg gtg aca gat ttc 48  
 Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe  
 1 5 10 15

140/261

att ctt ctg ggt ttg tct cac ccc cca aat cta aga agc ctc ctc ttc	96
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe	
20 25 30	
ctg gtc ttc ttc atc att tac atc ctc act cag ctg ggg aac ctg ctc	144
Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu	
35 40 45	
att ctg ctc acc atg tgg gct gac ccg aag ctc tgt gct cgc ccc atg	192
Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met	
50 55 60	
tac att ctt ctg gga gtg ctc tca ttc ctg gac atg tgg ctc tcc tca	240
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser	
65 70 75 80	
gtc acc gtt cct cgg ctt att ttg gat ttt act cct tcc atc aag gct	288
Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala	
85 90 95	
atc ccg ttt ggt ggc tgt gtg gct caa ctg tat ttc ttt cac ttc ctg	336
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu	
100 105 110	
ggc agc acc cag tgc ttc ctc tac acc ttg atg gcc tat gac agg tac	384
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr	
115 120 125	
cta gca ata tgt cag ccc ctg cac tac cca gtg ctc atg aat ggg agg	432
Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg	
130 135 140	
tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc atg cat	480
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His	
145 150 155 160	
ggg tct atc cag gcc acc ttg acc ttc cgc ctg ccc tac tgt ggg ccc	528
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro	
165 170 175	
aat cag gtg gat tac ttt atc tgt gac atc cgc gca gta ttg aga ctg	576
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu	
180 185 190	
gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc	624
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val	
195 200 205	
agg gta gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcc tat gcc	672
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala	
210 215 220	
aac ata gtc cat gcc atc ctg aag ata cgc acc gct gat ggg agg cgc	720
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg	
225 230 235 240	
cgg gcc ttc tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac	768
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr	
245 250 255	

141/261

tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa gac ccc 816  
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro  
                   260                  265                  270

ctg gat ggg gca gcg gct gtg ttt tac act gtt gtc act cca tta ctg 864  
 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu  
                   275                  280                  285

aac ccc ctc atc tat aca ctg agg aac cag gaa gtg aag tct gcc ctg 912  
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu  
                   290                  295                  300

aag agg ata aca gca gcg att cac atc tgc tct aaa tgg 951  
 Lys Arg Ile Thr Ala Ile His Ile Cys Ser Lys Trp  
                   305                  310                  315

&lt;210&gt; 124

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe  
 1                  5                  10                  15  
 Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe  
                   20                  25                  30  
 Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu  
                   35                  40                  45  
 Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met  
                   50                  55                  60  
 Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser  
                   65                  70                  75                  80  
 Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala  
                   85                  90                  95  
 Ile Pro Phe Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu  
                   100                  105                  110  
 Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr  
                   115                  120                  125  
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg  
                   130                  135                  140  
 Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His  
                   145                  150                  155                  160  
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro  
                   165                  170                  175  
 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu  
                   180                  185                  190  
 Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val  
                   195                  200                  205  
 Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala  
                   210                  215                  220  
 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg  
                   225                  230                  235                  240  
 Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr  
                   245                  250                  255  
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro  
                   260                  265                  270  
 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu  
                   275                  280                  285  
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu  
                   290                  295                  300

142/261

Lys Arg Ile Thr Ala Ala Ile His Ile Cys Ser Lys Trp  
 305 310 315

<210> 125  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

<400> 125  
 atg ccc aat tca acc acc gtg atg gaa ttt ctc ctc atg agg ttt tct 48  
 Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser  
 1 5 10 15  
 gat gtg tgg aca cta cag att tta cat tct gca tcc ttc ttt atg ttg 96  
 Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu  
 20 25 30  
 tat ttg gta act cta atg gga aac atc ctc att gtg acc gtc acc acc 144  
 Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Thr  
 35 40 45  
 tgt gac agc agc ctt cac atg ccc atg tac ttc ttc ctc agg aat ctc 192  
 Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu  
 50 55 60  
 cac ctt tcc tta att gac atg atg tat att tcc act att gtg cct aag 240  
 His Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys  
 65 70 75 80  
 atg ctg gtt aat tac ctg ctg gat caa agg acc att tcc ttt gtg ggg 288  
 Met Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly  
 85 90 95  
 tgc aca gct caa cac ttc ctc tac ctt acc ctt gtg gga gct gaa ttc 336  
 Cys Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe  
 100 105 110  
 ttc ctg ctg ggc ctc atg gcc tat gac cgc tat gtg gcc att tgc aac 384  
 Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 cct ctg aga tac cct gtc ctc atg agc cgc cgg gtc tgt tgg atg att 432  
 Pro Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile  
 130 135 140  
 ata gca ggt tcc tgg ttt ggg ggc tct ttg gat ggc ttc ctc cta acc 480  
 Ile Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr  
 145 150 155 160  
 ccc atc acc atg agc ttt ccc ttc tgc aat tcc cgg gag att aac cac 528  
 Pro Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His  
 165 170 175  
 ttc ttc tgt gag gca cca gca gtc ctg aag ttg gca tgt gca gac aca 576  
 Phe Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr  
 180 185 190

143/261

gcc ctc tac gag aca gtg atg tat gtg tgc tgt gtt ttg atg ctg ctg 624  
 Ala Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu  
 195 200 205

att cct ttc tct gta gtc ctt gct tcc tat gcc cga atc ctg act aca 672  
 Ile Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr  
 210 215 220

gtt cag tgc atg agc tca gtg gag ggc agg aag aag gca ttt gcc act 720  
 Val Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr  
 225 230 235 240

tgc tca tcc cac atg act gtg gtg tcc ttg ttc tac ggg gct gcc atg 768  
 Cys Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met  
 245 250 255

tac acc tac atg ctg cca cat tct tac cac aag cca gcc cag gac aaa 816  
 Tyr Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys  
 260 265 270

gtc ctc tct gtg ttt tac acc att ctc aca ccc atg ctg aac ccc ctc 864  
 Val Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu  
 275 280 285

atc tac agc ctt aga aac aag gat gtg act gga gct ctg aag agg gcc 912  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala  
 290 295 300

ttg ggg agg ttc aag ggt cct caa agg gtg 942  
 Leu Gly Arg Phe Lys Gly Pro Gln Arg Val  
 305 310

&lt;210&gt; 126

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser  
 1 5 10 15  
 Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu  
 20 25 30  
 Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr  
 35 40 45  
 Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu  
 50 55 60  
 His Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly  
 85 90 95  
 Cys Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe  
 100 105 110  
 Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile  
 130 135 140  
 Ile Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr  
 145 150 155 160  
 Pro Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His  
 165 170 175

144/261

Phe Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr  
                   180                  185                  190  
 Ala Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu  
                   195                  200                  205  
 Ile Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr  
                   210                  215                  220  
 Val Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr  
 225                  230                  235                  240  
 Cys Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met  
                   245                  250                  255  
 Tyr Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys  
                   260                  265                  270  
 Val Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala  
                   290                  295                  300  
 Leu Gly Arg Phe Lys Gly Pro Gln Arg Val  
 305                  310

&lt;210&gt; 127

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (942)

&lt;400&gt; 127

atg gca tgg gag aat cag acc ttc aac tcc gac ttc atc ctc ctt gga 48  
 Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly  
   1                  5                  10                  15  
  
 atc ttc aat cac agc cca cca cac acg ttc ctc ttc ttt ctg gtc ctg 96  
 Ile Phe Asn His Ser Pro Pro His Thr Phe Leu Phe Phe Leu Val Leu  
                   20                  25                  30  
  
 ggc atc ttt tta gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc 144  
 Gly Ile Phe Leu Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu  
                   35                  40                  45  
  
 atc tac ctg gac acc cag ctc cac acc ccc atg tac ttc ctc ctc agc 192  
 Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
                   50                  55                  60  
  
 caa ctg tcc ctc atg gac ctc atg ctc atc tgc acc acc gta ccc aag 240  
 Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys  
                   65                  70                  75                  80  
  
 atg gcc ttc aac tac ttg tct ggc agc aag tcc att tct atg gct ggt 288  
 Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly  
                   85                  90                  95  
  
 tgt gtc aca caa att ttc ttc tat ata tca ctg tct ggc tct gaa tgt 336  
 Cys Val Thr Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys  
                   100                  105                  110  
  
 ttt ctt ttg gct gtt atg gct tat gac cgc tat att gct att tgc cac 384  
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His  
                   115                  120                  125

145/261

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cct cta aga tat acc aat ctc atg aat cct aaa att tgt gga ctt atg 432
Pro Leu Arg Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met
130 135 140

gct acc ttc tcc tgg atc ctg ggc tct aca gat gga atc att gat gct 480
Ala Thr Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala
145 150 155 160

gta gcc aca ttt tcc ttc tcc ttt tgt ggg tct cgg gaa ata gcc cac 528
Val Ala Thr Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His
165 170 175

ttc ttc tgt gaa ttc cct tcc cta cta atc ctc tca tgc aat gac aca 576
Phe Phe Cys Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr
180 185 190

tca ata ttt gaa gag gtt att ttc atc tgc tgt ata gta atg ctt gtt 624
Ser Ile Phe Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val
195 200 205

ttc cct gtt gca atc atc att gct tcc tat gct gga gtt att ctg gct 672
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala
210 215 220

gtc att cac atg gga tct gga gag ggt cgt cgc aaa act ttc acg acc 720
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Thr Phe Thr Thr
225 230 235 240

tgt tcc tct cac ctc atg gtg gtg gga atg tac tat gga gca gct ttg 768
Cys Ser Ser His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
245 250 255

ttc atg tac ata cgg ccc aca tct gat cac tcc cca acg cag gac aag 816
Phe Met Tyr Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys
260 265 270

atg gtg tct gta ttc tac acc atc ctc act ccc atg ctg aat ccc ctc 864
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
275 280 285

atc tac agc ctc cgc aac aag gag gtg act aga gca ttc atg aag atc 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile
290 295 300

tta gga aag ggc aag tct gag agt gag tta 942
Leu Gly Lys Gly Lys Ser Glu Ser Glu Leu
305 310

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<210> 128  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 128
Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
1 5 10 15
Ile Phe Asn His Ser Pro Pro His Thr Phe Leu Phe Phe Leu Val Leu
20 25 30
Gly Ile Phe Leu Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
35 40 45

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146/261

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Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50          55          60
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
65          70          75          80
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
          85          90          95
Cys Val Thr Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met
          130          135          140
Ala Thr Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala
145          150          155          160
Val Ala Thr Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His
          165          170          175
Phe Phe Cys Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr
          180          185          190
Ser Ile Phe Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val
          195          200          205
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala
          210          215          220
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Thr Phe Thr Thr
225          230          235          240
Cys Ser Ser His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
          245          250          255
Phe Met Tyr Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys
          260          265          270
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile
          290          295          300
Leu Gly Lys Gly Lys Ser Glu Ser Glu Leu
305          310

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<210> 129  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(942)

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<400> 129
atg gca agg gag aat tcg acc ttc aac tcc gac ttc atc ctc ctg gga   48
Met Ala Arg Glu Asn Ser Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
 1          5          10          15

atc ttc aat cac agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg   96
Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
          20          25          30

gcc atc ttt tca gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc   144
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
          35          40          45

atc tac ctg gac acc cag ctc cac acc ccc atg tac ctc ctc ctc agc   192
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Leu Leu Leu Ser
          50          55          60

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147/261

caa ctg tcc ctc atg gac ctc atg ctc atc tgc acc acc gta ccc aag	240
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys	
65 70 75 80	
atg gcc ttc aac tac ctg tct ggc agc aag tcc att tct atg gct ggt	288
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly	
85 90 95	
tgt gcc aca caa att ttc ttc tat aca tca ctg ctt ggc tct gag tgc	336
Cys Ala Thr Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys	
100 105 110	
ttt ctt ttg gct gtt atg gct tat gac cgc tac act gcc att tgc cac	384
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His	
115 120 125	
cct cta aga tac acc aat ctc atg agc cct aaa att tgt gga ctt atg	432
Pro Leu Arg Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met	
130 135 140	
act gcc ttt tcc tgg atc ctg ggc tct acg gat gga att att gat gtt	480
Thr Ala Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Val	
145 150 155 160	
gta gca aca ttt tcc ttc tcc tac tgt ggg tct cgg gaa ata gcc cac	528
Val Ala Thr Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His	
165 170 175	
ttc ttc tgt gac ttc ccc tcc cta cta atc ctc tca tgc agt gac aca	576
Phe Phe Cys Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr	
180 185 190	
tca ata ttt gaa aag att ctt ttc atc tgc tgt ata gta atg att gtt	624
Ser Ile Phe Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val	
195 200 205	
ttc cct gtt gca atc atc att gct tcc tat gct cga gtt atc ctg gct	672
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala	
210 215 220	
gtc att cac atg gga tct gga gag ggt cgt cgc aaa gct ttt act act	720
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr	
225 230 235 240	
tgt tcc tct cac ctc ttg gtg gtg gga atg tac tat gga gca gct ttg	768
Cys Ser Ser His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu	
245 250 255	
ttc atg tac ata cgg ccc aca tct gat cgc tcc cca aca cag gac aag	816
Phe Met Tyr Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys	
260 265 270	
atg gtg tct gta ttc tac acc atc ctc act ccc atg ttg aat ccc ctc	864
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu	
275 280 285	
atc tac agc ctc cgc aac aag gag gtg acc aga gca ttc atg aag atc	912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile	
290 295 300	
tta gga aag ggc aac ata agt tca tca ata	942

148/261

Leu Gly Lys Gly Asn Ile Ser Ser Ser Ile  
305 310

<210> 130  
<211> 314  
<212> PRT  
<213> Homo sapiens

<400> 130  
Met Ala Arg Glu Asn Ser Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly  
1 5 10 15  
Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu  
20 25 30  
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu  
35 40 45  
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Leu Leu Leu Ser  
50 55 60  
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys  
65 70 75 80  
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly  
85 90 95  
Cys Ala Thr Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys  
100 105 110  
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His  
115 120 125  
Pro Leu Arg Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met  
130 135 140  
Thr Ala Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Val  
145 150 155 160  
Val Ala Thr Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His  
165 170 175  
Phe Phe Cys Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr  
180 185 190  
Ser Ile Phe Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val  
195 200 205  
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala  
210 215 220  
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr  
225 230 235 240  
Cys Ser Ser His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu  
245 250 255  
Phe Met Tyr Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys  
260 265 270  
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu  
275 280 285  
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile  
290 295 300  
Leu Gly Lys Gly Asn Ile Ser Ser Ser Ile  
305 310

<210> 131  
<211> 942  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (942)

<400> 131

149/261

atg gaa cag gat aat aca aca ttg ctg aca gag ttt gtt ctc aca gga	48
Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly	
1 5 10 15	
ctt aca tat cag cca gag tgg aaa atg ccc ctg ttc ttg gtg ttc ttg	96
Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu Phe Leu Val Phe Leu	
20 25 30	
gtg atc tat ctc atc act att gtg tgg aac ctt ggt ctg att gct ctt	144
Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu Gly Leu Ile Ala Leu	
35 40 45	
atc tgg aat gac cca caa ctt cac atc ccc atg tac ttt ttt ctt ggg	192
Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met Tyr Phe Phe Leu Gly	
50 55 60	
agt tta gcc ttt gtt gat gct tgg ata tct tcc aca gta act ccc aaa	240
Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys	
65 70 75 80	
atg ttg gtt aat ttc ttg gcc aaa aac agg atg ata tct ctg tct gaa	288
Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met Ile Ser Leu Ser Glu	
85 90 95	
tgc atg att caa ttt ttt tcc ttt gca ttt ggt gga act aca gaa tgt	336
Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly Gly Thr Thr Glu Cys	
100 105 110	
ttt ctc ttg gca aca atg gca tat gat cgc tat gta gcc ata tgc aaa	384
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys	
115 120 125	
cct tta cta tat cca gtg att atg aac aat tca cta tgc ata cgg ctg	432
Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser Leu Cys Ile Arg Leu	
130 135 140	
tta gcc ttc tca ttt tta ggt ggc ttc ctc cat gcc tta att cat gaa	480
Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His Ala Leu Ile His Glu	
145 150 155 160	
gtc ctt ata ttc aga tta acc ttc tgc aat tct aac ata ata cat cat	528
Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His	
165 170 175	
ttt tac tgt gat att ata cca ctg ttt atg att tcc tgt act gac cct	576
Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile Ser Cys Thr Asp Pro	
180 185 190	
tct att aat ttt cta atg gtt ttt att ttg tct ggc tca att cag gta	624
Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser Gly Ser Ile Gln Val	
195 200 205	
ttc acc att gtg aca gtt ctt aat tct tac aca ttt gct ctt ttc aca	672
Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr Phe Ala Leu Phe Thr	
210 215 220	
atc cta aaa aag aag tct gtt aga ggc gta agg aaa gcc ttt tcc acc	720
Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg Lys Ala Phe Ser Thr	
225 230 235 240	

150/261

tgt gga gcc cat ctc tta tct gtc tct tta tat tat ggc cca ctt atc 768  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Ile  
 245 250 255  
  
 ttc atg tat ttg cgc cct gca tct cca caa gca gat gac caa gat atg 816  
 Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
 260 265 270  
  
 ata gac tct gtc ttt tat aca atc ata att cct ttg cta aat ccc att 864  
 Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Ile  
 275 280 285  
  
 atc tac agt ctg aga aat aaa caa gta ata gat tca ttc aca aaa atg 912  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met  
 290 295 300  
  
 gta aaa aga aat caa aag cat tct tca aat 942  
 Val Lys Arg Asn Gln Lys His Ser Ser Asn  
 305 310

&lt;210&gt; 132

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu Phe Leu Val Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu Gly Leu Ile Ala Leu  
 35 40 45  
 Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met Ile Ser Leu Ser Glu  
 85 90 95  
 Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly Gly Thr Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser Leu Cys Ile Arg Leu  
 130 135 140  
 Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His Ala Leu Ile His Glu  
 145 150 155 160  
 Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His  
 165 170 175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile Ser Cys Thr Asp Pro  
 180 185 190  
 Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser Gly Ser Ile Gln Val  
 195 200 205  
 Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr Phe Ala Leu Phe Thr  
 210 215 220  
 Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Ile  
 245 250 255  
 Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
 260 265 270

151/261

Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met  
 290 295 300  
 Val Lys Arg Asn Gln Lys His Ser Ser Asn  
 305 310

<210> 133  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(951)

<400> 133  
 atg gag ccg ctc aac aga aca gag gtg tcc gag ttc ttt ctg aaa gga 48  
 Met Glu Pro Leu Asn Arg Thr Glu Val Ser Glu Phe Phe Leu Lys Gly  
 1 5 10 15  
 ttt tct ggc tac cca gcc ctg gag cat ctg ctc ttc cct ctg tgc tca 96  
 Phe Ser Gly Tyr Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser  
 20 25 30  
 gcc atg tac ctg gtg acc ctc ctg ggg aac aca gcc atc atg gcg gtg 144  
 Ala Met Tyr Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val  
 35 40 45  
 agc gtg cta gat atc cac ctg cac acg ccc gtg tac ttc ttc ctg ggc 192  
 Ser Val Leu Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly  
 50 55 60  
 aac ctc tct acc ctg gac atc tgc tac acg ccc acc ttt gtg cct ctg 240  
 Asn Leu Ser Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu  
 65 70 75 80  
 atg ctg gtc cac ctc ctg tca tcc cgg aag acc atc tcc ttt gct agg 288  
 Met Leu Val His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Arg  
 85 90 95  
 acc att tcc ttc cct ggc tgt gcc ctg cag atg tac ctg acc ctg gcg 336  
 Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr Leu Thr Leu Ala  
 100 105 110  
 ctg gga tca acg gag tgc ctg ctg ctg gct gtg atg gca tat gac cgt 384  
 Leu Gly Ser Thr Glu Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg  
 115 120 125  
 tat gtg gct atc tgc cag ccg ctt agg tac cca gag ctc atg agt ggg 432  
 Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu Leu Met Ser Gly  
 130 135 140  
 cag acc tgc atg cag atg gca gcg ctg agc tgg ggg aca ggc ttt gcc 480  
 Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly Thr Gly Phe Ala  
 145 150 155 160  
 aac tca ctg cta cag tcc atc ctt gtc tgg cac ctc ccc ttc tgt ggc 528  
 Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu Pro Phe Cys Gly  
 165 170 175

152/261

cac gtc atc aac tac ttc tat gag atc ttg gca gtg cta aaa ctg gcc 576  
 His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val Leu Lys Leu Ala  
 180 185 190

tgt ggg gac atc tcc ctc aat gcg ctg gca tta atg gtg gcc aca gcc 624  
 Cys Gly Asp Ile Ser Leu Asn Ala Leu Ala Leu Met Val Ala Thr Ala  
 195 200 205

gtc ctg aca ctg gcc ccc ctc ttg ctc atc tgc ctg tct tac ctt ttc 672  
 Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu Ser Tyr Leu Phe  
 210 215 220

atc ctg tct gcc atc ctt agg gta ccc tct gct gca ggc cgg tgc aaa 720  
 Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala Gly Arg Cys Lys  
 225 230 235 240

gcc ttc tcc acc tgc tca gcc cac cgc aca gtg gtg gtg gtt ttt tat 768  
 Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val Val Val Phe Tyr  
 245 250 255

ggg aca atc tcc ttc atg tac ttc aaa ccc aag gcc aag gat ccc aac 816  
 Gly Thr Ile Ser Phe Met Tyr Phe Lys Pro Lys Ala Lys Asp Pro Asn  
 260 265 270

gtg gat aag act gtc gca ttg ttc tac ggg gtt gtg acg ccc tgc ctg 864  
 Val Asp Lys Thr Val Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu  
 275 280 285

aac ccc atc att tac agc ctg agg aat gca gag gtg aaa gct gcc gtc 912  
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Ala Ala Val  
 290 295 300

cta act ctg ctg aga gga ggt ttg ctc tcc agg aaa gca 951  
 Leu Thr Leu Leu Arg Gly Gly Leu Leu Ser Arg Lys Ala  
 305 310 315

&lt;210&gt; 134

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

Met Glu Pro Leu Asn Arg Thr Glu Val Ser Glu Phe Phe Leu Lys Gly  
 1 5 10 15

Phe Ser Gly Tyr Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser  
 20 25 30

Ala Met Tyr Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val  
 35 40 45

Ser Val Leu Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly  
 50 55 60

Asn Leu Ser Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu  
 65 70 75 80

Met Leu Val His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Arg  
 85 90 95

Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr Leu Thr Leu Ala  
 100 105 110

Leu Gly Ser Thr Glu Cys Leu Leu Ala Val Met Ala Tyr Asp Arg  
 115 120 125

Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu Leu Met Ser Gly  
 130 135 140

153/261

Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly Thr Gly Phe Ala  
 145 150 155 160  
 Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu Pro Phe Cys Gly  
 165 170 175  
 His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val Leu Lys Leu Ala  
 180 185 190  
 Cys Gly Asp Ile Ser Leu Asn Ala Leu Met Val Ala Thr Ala  
 195 200 205  
 Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu Ser Tyr Leu Phe  
 210 215 220  
 Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala Gly Arg Cys Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val Val Val Phe Tyr  
 245 250 255  
 Gly Thr Ile Ser Phe Met Tyr Phe Lys Pro Lys Ala Lys Asp Pro Asn  
 260 265 270  
 Val Asp Lys Thr Val Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Ala Ala Val  
 290 295 300  
 Leu Thr Leu Leu Arg Gly Gly Leu Leu Ser Arg Lys Ala  
 305 310 315

<210> 135  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (957)

<400> 135  
 atg gca tgg gag aat cag acc ttc aac tct gac ttc ctc ctc ctg gga 48  
 Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 atc ttc aat cat agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg 96  
 Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu  
 20 25 30  
 gcc atc ttt tca gtg gcc ttc atg gga aac tcc atc atg gtt ctc ctc 144  
 Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Ile Met Val Leu Leu  
 35 40 45  
 atc tac ctg gat acc cag ctc cac acc ccc atg tac ttc ctc ctc agc 192  
 Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 caa ctg tcc ctc atg gac ctc atg ctc atc tgc acc act gta ccc aag 240  
 Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys  
 65 70 75 80  
 atg gcc ttc aac tac ttg tct ggc agc aag tcc att tct atg gct ggc 288  
 Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly  
 85 90 95  
 tgt gcc aca caa att ttc ttc tat ata tca ttg ctt ggc tcc gaa tgc 336  
 Cys Ala Thr Gln Ile Phe Phe Tyr Ile Ser Leu Leu Gly Ser Glu Cys  
 100 105 110

154/261

```

ttt ctg ttg gct tgc ttc ctc tta gca gcc atg gcc tat gac cgc tat 384
Phe Leu Leu Ala Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115                      120                      125

gcg gct gtc tgc cac cca ctc cga tat ccc act ctc atg agc tgg cag 432
Ala Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln
      130                      135                      140

ctg tgc ctg agg atg acc atg tgc tcc tgg ctc ctg ggt gca gct gac 480
Leu Cys Leu Arg Met Thr Met Ser Ser Trp Leu Leu Gly Ala Ala Asp
145                      150                      155                      160

ggc ctc ctg cag gct gtt gct acc ctg agc ttc cca tat tgc ggt gca 528
Gly Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala
      165                      170                      175

cac gag atc gat cac ttc ttc tgc gag gcc ccc gtg ttg gtg cgt ttg 576
His Glu Ile Asp His Phe Phe Cys Glu Ala Pro Val Leu Val Arg Leu
      180                      185                      190

gct tgt gct gac act tca gtc ttc gaa aac gcc atg tac atc tgc tgt 624
Ala Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys
      195                      200                      205

gtg tta atg ctc ctg gtc ccc ttt tcc ctc atc ctg tcc tcc tat ggt 672
Val Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly
      210                      215                      220

ctc atc ctc gct gct gtt ctg ctc atg cgc tct aca gaa gcc cgc aag 720
Leu Ile Leu Ala Ala Val Leu Leu Met Arg Ser Thr Glu Ala Arg Lys
225                      230                      235                      240

aag gcc ttt gcc acc tgc tct tca cat gtg gct gtg gtg gga ctc ttt 768
Lys Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe
      245                      250                      255

tat gga gct ggc att ttt acc tat atg aga ccc aaa tcc cac agg tcc 816
Tyr Gly Ala Gly Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser
      260                      265                      270

act aac cac gat aag gtt gtg tca gcc ttc tat act atg ttc acc cct 864
Thr Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro
      275                      280                      285

tta cta aat ccc ctc atc tac agt gtg agg aac agt gag gtc aag gaa 912
Leu Leu Asn Pro Leu Ile Tyr Ser Val Arg Asn Ser Glu Val Lys Glu
      290                      295                      300

gcc ctg aaa cgg tgg ctg ggg acg tgt gta aac cta aaa cac cag 957
Ala Leu Lys Arg Trp Leu Gly Thr Cys Val Asn Leu Lys His Gln
305                      310                      315

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&lt;210&gt; 136

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

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Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Leu Leu Leu Gly
 1                      5                      10                      15

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155/261

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Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
      20      25      30
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Ile Met Val Leu Leu
      35      40      45
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
      50      55      60
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
      65      70      75      80
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
      85      90      95
Cys Ala Thr Gln Ile Phe Phe Tyr Ile Ser Leu Leu Gly Ser Glu Cys
      100      105      110
Phe Leu Leu Ala Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115      120      125
Ala Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln
      130      135      140
Leu Cys Leu Arg Met Thr Met Ser Ser Trp Leu Leu Gly Ala Ala Asp
      145      150      155      160
Gly Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala
      165      170      175
His Glu Ile Asp His Phe Phe Cys Glu Ala Pro Val Leu Val Arg Leu
      180      185      190
Ala Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys
      195      200      205
Val Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly
      210      215      220
Leu Ile Leu Ala Ala Val Leu Leu Met Arg Ser Thr Glu Ala Arg Lys
      225      230      235      240
Lys Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe
      245      250      255
Tyr Gly Ala Gly Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser
      260      265      270
Thr Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro
      275      280      285
Leu Leu Asn Pro Leu Ile Tyr Ser Val Arg Asn Ser Glu Val Lys Glu
      290      295      300
Ala Leu Lys Arg Trp Leu Gly Thr Cys Val Asn Leu Lys His Gln
      305      310      315

```

&lt;210&gt; 137

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (939)

&lt;400&gt; 137

```

gcc agt ggc aac cac acc cca gtc acc aag ttc atc ttg cag gga ttc      48
Ala Ser Gly Asn His Thr Pro Val Thr Lys Phe Ile Leu Gln Gly Phe
  1              5              10              15

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```

tcc aat tat cca gac ctc cag gag ctt ctc ttc gga gcc atc ctg ctc      96
Ser Asn Tyr Pro Asp Leu Gln Glu Leu Leu Phe Gly Ala Ile Leu Leu
      20              25              30

```

```

atc tat gcc ata aca gtg gtg ggc aac ttg gga atg atg gca ctc atc      144
Ile Tyr Ala Ile Thr Val Val Gly Asn Leu Gly Met Met Ala Leu Ile
      35              40              45

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156/261

ttc aca gac tcc cat ctc caa agc cca atg tat ttc ttc ctc aat gtc	192
Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr Phe Phe Leu Asn Val	
50 55 60	
ctc tgc ttt ctt gat att tgt tac tct tct gtg gtc aca cct aag ctc	240
Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Val Thr Pro Lys Leu	
65 70 75 80	
ttg gtc aac ttc ctg gtc tct gac aag tcc atc tct ttt gag ggc tgt	288
Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile Ser Phe Glu Gly Cys	
85 90 95	
gtg gtc cag ctc gcc ttc ttt gta gtg cat gtg aca gct gag agc ttc	336
Val Val Gln Leu Ala Phe Phe Val Val His Val Thr Ala Glu Ser Phe	
100 105 110	
ctg ctg gcc tcc atg gcc tat gac cgc ttc cta gcc atc tgt caa ccc	384
Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro	
115 120 125	
ctc cat tat ggt tct atc atg acc agg ggg acc tgt ctc cag ctg gta	432
Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr Cys Leu Gln Leu Val	
130 135 140	
gct gtg tcc tat gca ttt ggt gga gcc aac tcc gct atc cag act gga	480
Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser Ala Ile Gln Thr Gly	
145 150 155 160	
aat gtc ttt gcc ctg cct ttc tgt ggg ccc aac cag cta aca cac tac	528
Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn Gln Leu Thr His Tyr	
165 170 175	
tac tgt gac ata cca ccc ctt ctc cac ctg gct tgt gcc aac aca gcc	576
Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala Cys Ala Asn Thr Ala	
180 185 190	
aca gca aga gtg gtc ctc tat gtc ttt tct gct ctg gtc acc ctt ctg	624
Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala Leu Val Thr Leu Leu	
195 200 205	
cct gct gca gtc att ctc acc tcc tac tgc ttg gtc ttg gtg gcc att	672
Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu Val Leu Val Ala Ile	
210 215 220	
ggg agg atg cgc tca gta gca ggg agg gag aag gac ctc tcc act tgt	720
Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys Asp Leu Ser Thr Cys	
225 230 235 240	
gcc tcc cac ttt ctg gcc att gcc att ttc tat ggc act gtg gtt ttc	768
Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr Gly Thr Val Val Phe	
245 250 255	
acc tat gtt cag ccc cat gga tct act aac aat acc aat ggc caa gta	816
Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn Thr Asn Gly Gln Val	
260 265 270	
gtg tcc gtc ttc tac acc atc ata att ccc atg ctc aat ccc ttc atc	864
Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met Leu Asn Pro Phe Ile	
275 280 285	

157/261

tat agc ctc cgc aac aag gag gtg aag ggc gct ctg cag agg aag ctt 912  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gln Arg Lys Leu  
 290 295 300

cag aaa ttt gtt tgt cat agc aaa aaa 939  
 Gln Lys Phe Val Cys His Ser Lys Lys  
 305 310

<210> 138  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Ala Ser Gly Asn His Thr Pro Val Thr Lys Phe Ile Leu Gln Gly Phe  
 1 5 10 15  
 Ser Asn Tyr Pro Asp Leu Gln Glu Leu Phe Gly Ala Ile Leu Leu  
 20 25 30  
 Ile Tyr Ala Ile Thr Val Val Gly Asn Leu Gly Met Met Ala Leu Ile  
 35 40 45  
 Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr Phe Phe Leu Asn Val  
 50 55 60  
 Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Val Thr Pro Lys Leu  
 65 70 75 80  
 Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile Ser Phe Glu Gly Cys  
 85 90 95  
 Val Val Gln Leu Ala Phe Phe Val Val His Val Thr Ala Glu Ser Phe  
 100 105 110  
 Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro  
 115 120 125  
 Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr Cys Leu Gln Leu Val  
 130 135 140  
 Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser Ala Ile Gln Thr Gly  
 145 150 155 160  
 Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn Gln Leu Thr His Tyr  
 165 170 175  
 Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala Cys Ala Asn Thr Ala  
 180 185 190  
 Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala Leu Val Thr Leu Leu  
 195 200 205  
 Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu Val Leu Val Ala Ile  
 210 215 220  
 Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys Asp Leu Ser Thr Cys  
 225 230 235 240  
 Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr Gly Thr Val Val Phe  
 245 250 255  
 Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn Thr Asn Gly Gln Val  
 260 265 270  
 Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gln Arg Lys Leu  
 290 295 300  
 Gln Lys Phe Val Cys His Ser Lys Lys  
 305 310

<210> 139  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

158/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(939)

&lt;400&gt; 139

atg gag cag agc aat tat tcc gtg tat gcc gac ttt atc ctt ctg ggc	48
Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly	
1 5 10 15	
ctc atc acc cat cct gcc ttc ccc ggg ctt ctc ttt gca gta gtc ttc	96
Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Val Val Phe	
20 25 30	
tcc atc ttt gtg gtg gct ata aca gcc aac ttg gtc atg att ctg ctc	144
Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu Leu	
35 40 45	
atc cac atg gac tcc cgc ctc cac aca ccc atg tac ttc ttg ctc agc	192
Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser	
50 55 60	
cag ctc tcc atc atg gat acc atc tac atc tgt atc act gtc ccc aag	240
Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro Lys	
65 70 75 80	
atg ctc cag gac ctc ctg tcc aag gac aag acc att tcc ttc ctg ggc	288
Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu Gly	
85 90 95	
tgt gca gtt caa atc ttc tac ctg acc ctg att gga ggg gaa ttc ttc	336
Cys Ala Val Gln Ile Phe Tyr Leu Thr Leu Ile Gly Gly Glu Phe Phe	
100 105 110	
ctg ctg ggt ctc atg gcc tat gac cgc tat gtg gct gtg tgc aac cct	384
Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro	
115 120 125	
cta cgg tac cct ctc ctc atg aac cgc agg gtt tgc tta ttc atg gtg	432
Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe Met Val	
130 135 140	
gtc ggc tcc tgg gtt ggt ggt tcc ttg gat ggg ttc atg ctg act cct	480
Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu Thr Pro	
145 150 155 160	
gtc act atg agt ttc ccc ttc tgt aga tcc cga gag atc aat cac ttt	528
Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn His Phe	
165 170 175	
ttc tgt gag atc cca gcc gtg ctg aag ttg tct tgc aca gac acg tca	576
Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp Thr Ser	
180 185 190	
ctc tat gag acc ctg atg tat gcc tgc tgc gtg ctg atg ctg ctt atc	624
Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu Leu Ile	
195 200 205	
cct cta tct gtc atc tct gtg tcc tac acg cac atc ctc ctg act gtc	672
Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu Thr Val	
210 215 220	
cac agg atg aac tct gct gag ggc cgg cgc aaa gcc ttt gct acg tgt	720

159/261

His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 tcc tcc cac att atg gtg gtg agc gtt ttc tac ggg gca gcc ttc tac 768  
 Ser Ser His Ile Met Val Val Ser Val Phe Tyr Gly Ala Ala Phe Tyr  
 245 250 255  
 acc aac gtg ctg ccc cac tcc tac cac act cca gag aaa gat aaa gtg 816  
 Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp Lys Val  
 260 265 270  
 gtg tct gcc ttc tac acc atc ctc acc ccc atg ctc aac cca ctc atc 864  
 Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 tac agc ttg agg aat aaa gat gtg gct gca gct ctg agg aaa gta cta 912  
 Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys Val Leu  
 290 295 300  
 ggg aga tgt ggt tcc tcc cag agc atc 939  
 Gly Arg Cys Gly Ser Ser Gln Ser Ile  
 305 310

<210> 140  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Val Val Phe  
 20 25 30  
 Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu Leu  
 35 40 45  
 Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Val Gln Ile Phe Tyr Leu Thr Leu Ile Gly Gly Glu Phe Phe  
 100 105 110  
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro  
 115 120 125  
 Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe Met Val  
 130 135 140  
 Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu Thr Pro  
 145 150 155 160  
 Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn His Phe  
 165 170 175  
 Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp Thr Ser  
 180 185 190  
 Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu Leu Ile  
 195 200 205  
 Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu Thr Val  
 210 215 220  
 His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ser Ser His Ile Met Val Val Ser Val Phe Tyr Gly Ala Ala Phe Tyr  
 245 250 255

160/261

Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp Lys Val  
 260 265 270  
 Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys Val Leu  
 290 295 300  
 Gly Arg Cys Gly Ser Ser Gln Ser Ile  
 305 310

<210> 141  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(957)

<400> 141  
 atg gca gag atg aac ctc acc ttg gtg acc gag ttc ctc ctt att gca 48  
 Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala  
 1 5 10 15  
 ttc act gaa tat cct gaa tgg gca ctc cct ctc ttc ctc ttg ttt tta 96  
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 ttt atg tat ctc atc acc gta ttg ggg aac tta gag atg att att ctg 144  
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu  
 35 40 45  
 atc ctc atg gat cac cag ctc cac gct cca atg tat ttc ctt ctg agt 192  
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 cac ctc gct ttc atg gac gtc tgc tac tca tct atc act gtc ccc cag 240  
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln  
 65 70 75 80  
 atg ctg gca gtg ctg ctg gag cat ggg gca gct tta tct tac aca cgc 288  
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg  
 85 90 95  
 tgt gct gct cag ttc ttt ctg ttc acc ttc ttt ggt tcc atc gac tgc 336  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys  
 100 105 110  
 tac ctc ttg gcc ctc atg gcc tat gac cgc tac ttg gct gtg tgc cag 384  
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln  
 115 120 125  
 ccc ctg ctt tat gtc acc atc ctg aca cag cag gcc cgc ttg agt ctt 432  
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu  
 130 135 140  
 gtg gct ggg gct tac gtt gct ggt ctc atc agt gcc ttg gtg cgg aca 480  
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr  
 145 150 155 160

161/261

tgc ctt tgt tgc acg gtc aca gcc ttc act ctc tcc ttt tgt gga aac 528  
 Cys Leu Cys Ser Thr Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn  
 165 170 175

aat gag atc aac ttc att ttc tgt gac ctc cct cct cta tta aaa ctc 576  
 Asn Glu Ile Asn Phe Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu  
 180 185 190

tcc tgt ggg gac agc tac act cag gaa gtg gtg att att gtg ttt gct 624  
 Ser Cys Gly Asp Ser Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala  
 195 200 205

ctt ttc gtc atg cct gcc tgt atc ttg gtg atc ttg gta tcc tac ctg 672  
 Leu Phe Val Met Pro Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu  
 210 215 220

ttt atc att gtg gcc atc ctg cag atc cac tct gct gga ggc cgg gcc 720  
 Phe Ile Ile Val Ala Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala  
 225 230 235 240

aag acc ttc tcc acc tgc gcc tcc cac ctc act gcc gtc gct ctt ttc 768  
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe  
 245 250 255

ttt ggc acc ctc atc ttc atg tac ctg cga gac aac aca ggc cag tcc 816  
 Phe Gly Thr Leu Ile Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser  
 260 265 270

tcc gag gga gac cga gtg gtg tct gtg ctc tac acg gtg gtg acc cca 864  
 Ser Glu Gly Asp Arg Val Val Ser Val Leu Tyr Thr Val Val Thr Pro  
 275 280 285

atg ctg aat ccc ctt atc tat agc ctg aga aac aag gag gta aaa gag 912  
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu  
 290 295 300

gcc act agg aaa gcc ctg agc aaa tca aag cct gct aga aga ccc 957  
 Ala Thr Arg Lys Ala Leu Ser Lys Ser Lys Pro Ala Arg Arg Pro  
 305 310 315

&lt;210&gt; 142

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala  
 1 5 10 15  
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu  
 35 40 45  
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln  
 65 70 75 80  
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg  
 85 90 95  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys  
 100 105 110

162/261

Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln  
 115 120 125  
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu  
 130 135 140  
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr  
 145 150 155 160  
 Cys Leu Cys Ser Thr Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn  
 165 170 175  
 Asn Glu Ile Asn Phe Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu  
 180 185 190  
 Ser Cys Gly Asp Ser Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala  
 195 200 205  
 Leu Phe Val Met Pro Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu  
 210 215 220  
 Phe Ile Ile Val Ala Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala  
 225 230 235 240  
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe  
 245 250 255  
 Phe Gly Thr Leu Ile Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser  
 260 265 270  
 Ser Glu Gly Asp Arg Val Val Ser Val Leu Tyr Thr Val Val Thr Pro  
 275 280 285  
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu  
 290 295 300  
 Ala Thr Arg Lys Ala Leu Ser Lys Ser Lys Pro Ala Arg Arg Pro  
 305 310 315

&lt;210&gt; 143

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(942)

&lt;400&gt; 143

atg aaa aca gga aat caa agt ttt ggg aca gat ttt cta ctt gtt ggt 48  
 Met Lys Thr Gly Asn Gln Ser Phe Gly Thr Asp Phe Leu Leu Val Gly  
 1 5 10 15  
 ctt ttc caa tat ggc tgg ata aac tct ctt ctc ttt gtc gtc att gcc 96  
 Leu Phe Gln Tyr Gly Trp Ile Asn Ser Leu Leu Phe Val Val Ile Ala  
 20 25 30  
 acc ctc ttt aca gtt gct ctg aca gga aat atc atg ctg atc cac ctc 144  
 Thr Leu Phe Thr Val Ala Leu Thr Gly Asn Ile Met Leu Ile His Leu  
 35 40 45  
 att cga ctg aac acc aga ctc cac act cca atg tac ttt ctg ctc agt 192  
 Ile Arg Leu Asn Thr Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 cag ctc tcc atc gtt gac ctc atg tac atc tcc acc aca gtg ccc aag 240  
 Gln Leu Ser Ile Val Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 atg gca gtc agc ttc ctc tca cag agt aag acc att aga ttt ttg ggc 288  
 Met Ala Val Ser Phe Leu Ser Gln Ser Lys Thr Ile Arg Phe Leu Gly  
 85 90 95



163/261

tgt gag att caa acg tat gtg ttc ttg gcc ctt ggt gga act gaa gcc	336
Cys Glu Ile Gln Thr Tyr Val Phe Leu Ala Leu Gly Gly Thr Glu Ala	
100 105 110	
ctt ctc ctt ggt ttt atg tct tat gat cgc tat gta gct atc tgt cac	384
Leu Leu Leu Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His	
115 120 125	
cct tta cat tat cct atg ctt atg agc aag aag atc tgc tgc ctc atg	432
Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys Cys Leu Met	
130 135 140	
gtt gca tgt gca tgg gcc agt ggt tct atc aat gct ttc ata cat aca	480
Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe Ile His Thr	
145 150 155 160	
ttg tat gtg ttt cag ctt cca ttc tgt agg tct cgg ctc att aac cac	528
Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu Ile Asn His	
165 170 175	
ttt ttc tgt gaa gtt cca gct cta cta tca ttg gtg tgt cag gac acc	576
Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys Gln Asp Thr	
180 185 190	
tcc cag tat gag tat aca gtc ctc ctg agt gga ctt att atc ttg cta	624
Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile Ile Leu Leu	
195 200 205	
cta cca ttc cta gcc att ctg gct tcc tat gct cgt gtg ctt att gtg	672
Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val Leu Ile Val	
210 215 220	
gta ttc cag atg agc tca gga aaa gga cag gca aaa gct gtt tcc act	720
Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala Val Ser Thr	
225 230 235 240	
tgt tcc tcc cac ctg att gtg gca agc ctg ttc tat gca acc act ctc	768
Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala Thr Thr Leu	
245 250 255	
ttt acc tac aca agg cca cac tcc ttg cgt tcc cct tca cgg gat aag	816
Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser Arg Asp Lys	
260 265 270	
gcg gtg gca gta ttt tac acc att gtc aca cct cta ctg aac cca ttt	864
Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu Asn Pro Phe	
275 280 285	
atc tac agc ctg aga aat aag gaa gtg acg ggg gca gtg agg aga ctg	912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val Arg Arg Leu	
290 295 300	
ttg gga tat tgg ata tgc tgt aga aaa tat	942
Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr	
305 310	

&lt;210&gt; 144

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

164/261

&lt;400&gt; 144

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Met Lys Thr Gly Asn Gln Ser Phe Gly Thr Asp Phe Leu Leu Val Gly
 1           5           10           15
Leu Phe Gln Tyr Gly Trp Ile Asn Ser Leu Leu Phe Val Val Ile Ala
      20           25           30
Thr Leu Phe Thr Val Ala Leu Thr Gly Asn Ile Met Leu Ile His Leu
      35           40           45
Ile Arg Leu Asn Thr Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
      50           55           60
Gln Leu Ser Ile Val Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys
      65           70           75           80
Met Ala Val Ser Phe Leu Ser Gln Ser Lys Thr Ile Arg Phe Leu Gly
      85           90           95
Cys Glu Ile Gln Thr Tyr Val Phe Leu Ala Leu Gly Gly Thr Glu Ala
      100          105          110
Leu Leu Leu Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys Cys Leu Met
      130          135          140
Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe Ile His Thr
      145          150          155          160
Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu Ile Asn His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys Gln Asp Thr
      180          185          190
Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile Ile Leu Leu
      195          200          205
Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val Leu Ile Val
      210          215          220
Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala Val Ser Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala Thr Thr Leu
      245          250          255
Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser Arg Asp Lys
      260          265          270
Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val Arg Arg Leu
      290          295          300
Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr
      305          310

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&lt;210&gt; 145

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(945)

&lt;400&gt; 145

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atg gaa agg aaa aac cgc ttt gct ttt gta aat gaa ttt ata ctc caa 48
Met Glu Arg Lys Asn Arg Phe Ala Phe Val Asn Glu Phe Ile Leu Gln
 1           5           10           15

ggt ttc tct tgt gag tgg aca att cag atc ttc ctc ttc tca ctc ttt 96
Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe
      20           25           30

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165/261

act aca aca tat gca ctg act ata aca ggg aat gga gcc att gct ttt	144
Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Phe	
35 40 45	
gtc ctg tgg tgt gac cgg cga ctt cac act ccc atg tac atg ttc ctg	192
Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr Met Phe Leu	
50 55 60	
gga aat ttc tcc ttt tta gag ata tgg tat gtc tct tct aca gtt ccc	240
Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro	
65 70 75 80	
aag atg ttg gtc aac ttc ctt tca gag aaa aaa aac atc tcc ttt gct	288
Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile Ser Phe Ala	
85 90 95	
gga tgt ttt ctc cag ttt tat ttc ttc ttc tct ttg ggt aca tca gaa	336
Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu	
100 105 110	
tgc ttg ctt ttg act gtg atg gcc ttt gat cag tac ctt gct atc tgc	384
Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Ala Ile Cys	
115 120 125	
cgt ccc ttg ctc tat cct aat atc atg act ggg cat ctc tat gcc aaa	432
Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu Tyr Ala Lys	
130 135 140	
ctg gtc ata ctg tgc tgg gtt tgt gga ttt ctg tgg ttc ctg atc ccc	480
Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro	
145 150 155 160	
att gtt ctc atc tct cag atg ccc ttc tgt ggc cca aac att att gac	528
Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Ile Asp	
165 170 175	
cat gtt gtg tgt gac cca ggg cca cga ttt gca ttg gat tgt gtt tct	576
His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp Cys Val Ser	
180 185 190	
gcc cca aga atc caa ctg ttt tgc tac act cta agc tca tta gtt att	624
Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile	
195 200 205	
ttt ggt aac ttc ctc ttt att att gga tcc tat act ctt gtc ctg aaa	672
Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys	
210 215 220	
gct atg ttg ggt atg cct tca agc act ggg aga cat aag gcc ttc tct	720
Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys Ala Phe Ser	
225 230 235 240	
acc tgt ggg tct cat ttg gct gtg gta tca ctg tgc tat agc tct ctt	768
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr Ser Ser Leu	
245 250 255	
atg gtc atg tat gtg agc cca gga ctc gga cat tct aca ggg atg cag	816
Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr Gly Met Gln	
260 265 270	

166/261

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aaa att gaa act ttg ttc tat gct atg gtg acc cca ctc ttc aat ccc 864
Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro
      275                      280                      285

ctt atc tat agc ctc cag aat aag gag ata aag gca gcc ctg agg aaa 912
Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys
      290                      295                      300

gtt ctg ggg aag aaa cag ttt tgc agc aaa atg 945
Val Leu Gly Lys Lys Gln Phe Cys Ser Lys Met
305                      310                      315

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<210> 146  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

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<400> 146
Met Glu Arg Lys Asn Arg Phe Ala Phe Val Asn Glu Phe Ile Leu Gln
 1          5          10          15
Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe
      20          25          30
Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Phe
      35          40          45
Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr Met Phe Leu
      50          55          60
Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro
      65          70          75          80
Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile Ser Phe Ala
      85          90          95
Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu
      100          105          110
Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Ala Ile Cys
      115          120          125
Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu Tyr Ala Lys
      130          135          140
Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro
      145          150          155          160
Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Ile Asp
      165          170          175
His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp Cys Val Ser
      180          185          190
Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile
      195          200          205
Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys
      210          215          220
Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys Ala Phe Ser
      225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr Ser Ser Leu
      245          250          255
Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr Gly Met Gln
      260          265          270
Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro
      275          280          285
Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys
      290          295          300
Val Leu Gly Lys Lys Gln Phe Cys Ser Lys Met
305                      310                      315

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&lt;210&gt; 147

167/261

<211> 933  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(933)

<400> 147  
 atg gat aaa aac caa aca gaa gtg atg aga gaa ttt ttc ttg tca ggg 48  
 Met Asp Lys Asn Gln Thr Glu Val Met Arg Glu Phe Phe Leu Ser Gly  
 1 5 10 15

ttc tca cag aca cca tct att gaa gca ggg cta ttt gta cta ttt ctt 96  
 Phe Ser Gln Thr Pro Ser Ile Glu Ala Gly Leu Phe Val Leu Phe Leu  
 20 25 30

ttc ttc tat atg tcc att tgg gtt ggc aat gtc ctc atc atg gtc aca 144  
 Phe Phe Tyr Met Ser Ile Trp Val Gly Asn Val Leu Ile Met Val Thr  
 35 40 45

gta gca tct gat aaa tac ctg aat tca tca ccc atg tat ttc ctt ctt 192  
 Val Ala Ser Asp Lys Tyr Leu Asn Ser Ser Pro Met Tyr Phe Leu Leu  
 50 55 60

ggc aac ctc tca ttt ctg gac cta tgt tat tca aca gta acg acc cct 240  
 Gly Asn Leu Ser Phe Leu Asp Leu Cys Tyr Ser Thr Val Thr Thr Pro  
 65 70 75 80

aag ctt ctg gct gac ttc ttt aat cat gaa aaa ctc att tcc tat gac 288  
 Lys Leu Leu Ala Asp Phe Phe Asn His Glu Lys Leu Ile Ser Tyr Asp  
 85 90 95

caa tgc att gtg caa ctc ttc ttc ctg cat ttt gta ggg gca gct gag 336  
 Gln Cys Ile Val Gln Leu Phe Phe Leu His Phe Val Gly Ala Ala Glu  
 100 105 110

atg ttc ctg ctc aca gtg atg gcg tac gat cgc tat gtt gca atc tgt 384  
 Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125

cgc ccg ctg cac tac acc act gtc atg agt cgg ggg tta tgc tgt gtg 432  
 Arg Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly Leu Cys Cys Val  
 130 135 140

ttg gtt gct gcc tcc tgg atg gga gga ttt gtg cac tcc act gtc cag 480  
 Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His Ser Thr Val Gln  
 145 150 155 160

acc att ctc act gtc cat cta ccc ttt tgt ggg cca aat cag gtg gaa 528  
 Thr Ile Leu Thr Val His Leu Pro Phe Cys Gly Pro Asn Gln Val Glu  
 165 170 175

aac act ttt ttt tgt gat gtt ccc cct gtc atc aaa ctt gct tgt gct 576  
 Asn Thr Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Ala  
 180 185 190

gac act ttt gtc att gaa ttg ctc atg gta tct aac agt ggg ttg atc 624  
 Asp Thr Phe Val Ile Glu Leu Met Val Ser Asn Ser Gly Leu Ile  
 195 200 205

[illegible]

<400>	148														
Met	Asp	Lys	Asn	Gln	Thr	Glu	Val	Met	Arg	Glu	Phe	Phe	Leu	Ser	Gly
1				5					10					15	
Phe	Ser	Gln	Thr	Pro	Ser	Ile	Glu	Ala	Gly	Leu	Phe	Val	Leu	Phe	Leu
			20					25					30		
Phe	Phe	Tyr	Met	Ser	Ile	Trp	Val	Gly	Asn	Val	Leu	Ile	Met	Val	Thr
		35					40					45			
Val	Ala	Ser	Asp	Lys	Tyr	Leu	Asn	Ser	Ser	Pro	Met	Tyr	Phe	Leu	Leu
	50					55					60				
Gly	Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Tyr	Ser	Thr	Val	Thr	Thr	Pro
65					70					75					80
Lys	Leu	Leu	Ala	Asp	Phe	Phe	Asn	His	Glu	Lys	Leu	Ile	Ser	Tyr	Asp
				85					90					95	
Gln	Cys	Ile	Val	Gln	Leu	Phe	Phe	Leu	His	Phe	Val	Gly	Ala	Ala	Glu
			100					105					110		
Met	Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
		115					120					125			
Arg	Pro	Leu	His	Tyr	Thr	Thr	Val	Met	Ser	Arg	Gly	Leu	Cys	Cys	Val
		130				135					140				
Leu	Val	Ala	Ala	Ser	Trp	Met	Gly	Gly	Phe	Val	His	Ser	Thr	Val	Gln
145					150					155					160
Thr	Ile	Leu	Thr	Val	His	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Gln	Val	Glu
				165					170					175	
Asn	Thr	Phe	Phe	Cys	Asp	Val	Pro	Pro	Val	Ile	Lys	Leu	Ala	Cys	Ala
			180					185					190		
Asp	Thr	Phe	Val	Ile	Glu	Leu	Leu	Met	Val	Ser	Asn	Ser	Gly	Leu	Ile
		195					200					205			

169/261

Ser Thr Ile Ser Phe Val Val Leu Ile Ser Ser Tyr Thr Thr Ile Leu  
 210 215 220  
 Val Lys Ile Arg Ser Lys Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Ala Arg Pro Phe Ser Thr Phe Ser Val Asp Lys Met Val Ser  
 260 265 270  
 Val Leu Tyr Asn Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Ser Ala Met Gln Lys Leu Trp Val Arg  
 290 295 300  
 Asn Gly Leu Thr Trp Lys Lys  
 305 310

<210> 149  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 149  
 atg cag agg agc aat cat aca gtg act gag ttt ata ctg ctg ggc ttc 48  
 Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 acc aca gac cca gga atg cag ctg ggc ctc ttc gtg gtg ttc ctg ggc 96  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 gtg tac tct ctc act gtg gta gga aat agc acc ctc atc gtg ttg atc 144  
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 tgt aat gac tcc tgc ctc cac aca ccc atg tat ttt ttc act gga aat 192  
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Thr Gly Asn  
 50 55 60  
 ctg tgc ttt ctg gat ctc tgg tat tct tct gtc tac acc cca aag atc 240  
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile  
 65 70 75 80  
 cta gtg acc tgc atc tct gaa gac aaa agc atc tcc ttt gct ggc tgc 288  
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
 85 90 95  
 ctg tgt cag ttc ttc ttc tct gca ggg ctg gcc tat agt gag tgc tac 336  
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr  
 100 105 110  
 ctg ctg gct gcc gtg gct tat gac cgc tac gtg gcc atc tcc aag ccc 384  
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro  
 115 120 125  
 ctg ctt tat gcc cag gcc atg tcc ata aag ctg tgt gca ttg ctg gta 432  
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val  
 130 135 140

170/261

gca gtc tca tat tgt ggt ggc ttt att aac tct tca atc atc acc aag 480  
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys  
 145 150 155 160

aaa acg ttt tcc ttt aac ttc tgc cgt gaa aac atc att gat gac ttt 528  
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe  
 165 170 175

ttc tgt gat ttg ctt ccc ttg gtg gag ctg gcc tgt ggc gag aag ggc 576  
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly  
 180 185 190

ggc tat aaa att atg atg tac ttc ctg ctg gcc tcc aat gtc atc tgc 624  
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys  
 195 200 205

ccc gca gtg ctc atc ctg gcc tcc tac ctc ttt atc atc acc agt gtc 672  
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val  
 210 215 220

ttg agg atc tcc tcc tcc aag ggc tac ctc aaa gcc ttc tcc aca tgc 720  
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys  
 225 230 235 240

tcc tcc cac ctg acc tct gtc act tta tac tat ggc tcc att ctc tac 768  
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr  
 245 250 255

atc tac gct ctc ccc aga tct agc tat tct ttt gat atg gac aaa ata 816  
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile  
 260 265 270

gtt tct aca ttt tac act gtg gta ttc ccc atg ttg aat ctc atg atc 864  
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile  
 275 280 285

tac agc cta agg aat aag gat gtg aaa gag gct ctg aaa aaa ctt ctc 912  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu  
 290 295 300

tcc cat aaa tca aga tta tct cca cca 939  
 Ser His Lys Ser Arg Leu Ser Pro Pro  
 305 310

&lt;210&gt; 150

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Thr Gly Asn  
 50 55 60  
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile  
 65 70 75 80



171/261

Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
                     85                    90                    95  
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr  
                     100                    105                    110  
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro  
                     115                    120                    125  
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val  
                     130                    135                    140  
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys  
                     145                    150                    155                    160  
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe  
                     165                    170                    175  
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly  
                     180                    185                    190  
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys  
                     195                    200                    205  
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val  
                     210                    215                    220  
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys  
                     225                    230                    235                    240  
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr  
                     245                    250                    255  
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile  
                     260                    265                    270  
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile  
                     275                    280                    285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu  
                     290                    295                    300  
 Ser His Lys Ser Arg Leu Ser Pro Pro  
                     305                    310

<210> 151  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 151  
 atg gca gaa gaa aat aag att ctg gtg act cac ttt gtc ctc aca gga 48  
 Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly  
   1                    5                    10                    15  
  
 ctc aca gat cat cca ggg ctg cag gcg ccc ctg ttc ctg gtg ttc ttg 96  
 Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu  
                     20                    25                    30  
  
 gtc atc tac ctc atc acc ctg gtg ggc aac ctt ggc ctg atg gct ctc 144  
 Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu  
                     35                    40                    45  
  
 atc tgg aag gac ccc cac ctt cac acc ccc ata tac tta ttt ctt ggc 192  
 Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly  
                     50                    55                    60  
  
 agt tta gcc ttt gca gat gca tgc act tca tcc tct gta act tct aag 240  
 Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys  
                     65                    70                    75                    80

172/261

atg ctt atc aat ttt ttt tta tca aag aat cat atg cta tcc atg gct	288
Met Leu Ile Asn Phe Phe Leu Ser Lys Asn His Met Leu Ser Met Ala	
85 90 95	
aag tgt gcc acc cag ttt tac ttt ttt ggt tcc aat gca acc aca gaa	336
Lys Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu	
100 105 110	
tgc ttc ctg ctg gta gtg atg gcc tat gac cgc tat gta gcc ata tgc	384
Cys Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys	
115 120 125	
aat ccc ttg ctt tat cca gtg gtg atg tcc aat agc ctc tgt act cag	432
Asn Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln	
130 135 140	
ttt ata ggt att tca tat ttt att ggt ttt ctg cat tca gcg att cat	480
Phe Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His	
145 150 155 160	
gtg ggt ttg tta ttt aga tta act ttc tgc agg tcc aat att ata cat	528
Val Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His	
165 170 175	
tat ttc tac tgt gaa att tta cag ctg ttc aaa att tct tgc acc aat	576
Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn	
180 185 190	
cct aca gtt aat ata ctt ctg att ttc atc ttt tca gca ttt ata caa	624
Pro Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln	
195 200 205	
gtc ttc act ttt atg act ctt atc gtc tct tac tcc tat att ctc tct	672
Val Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser	
210 215 220	
gcc atc ctg aaa aag aag tct gag aag ggt aga agc aaa gcc ttc tct	720
Ala Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser	
225 230 235 240	
act tgc agt gcc cat ctg ctc tct gtc tct ttg ttc tac ggc acc ctc	768
Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu	
245 250 255	
ttc ttc atg tat gtg agt tct agg tct gga tca gct gca gat cag gcc	816
Phe Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala	
260 265 270	
aaa atg tat tct tta ttt tac aca ata ata att cct tta cta aat cct	864
Lys Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro	
275 280 285	
ttt att tac agc cta agg aac aaa gag gtg cat agg tgc ata aga aac	912
Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val His Arg Cys Ile Arg Asn	
290 295 300	
tta ctg ata tgt aga ttc ata ttt ttt att tct	945
Leu Leu Ile Cys Arg Phe Ile Phe Phe Ile Ser	
305 310 315	

&lt;210&gt; 152

173/261

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

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Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1           5           10           15
Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
          20           25           30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
          35           40           45
Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
          50           55           60
Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
65           70           75           80
Met Leu Ile Asn Phe Phe Leu Ser Lys Asn His Met Leu Ser Met Ala
          85           90           95
Lys Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu
          100          105          110
Cys Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln
          130          135          140
Phe Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His
145          150          155          160
Val Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His
          165          170          175
Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn
          180          185          190
Pro Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln
          195          200          205
Val Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser
          210          215          220
Ala Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser
225          230          235          240
Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu
          245          250          255
Phe Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala
          260          265          270
Lys Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val His Arg Cys Ile Arg Asn
          290          295          300
Leu Leu Ile Cys Arg Phe Ile Phe Phe Ile Ser
305          310          315

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&lt;210&gt; 153

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(936)

&lt;400&gt; 153

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atg gtt ggg gca aat cac tcc gtg gtg tca gag ttt gtg ttc ctg gga 48
Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1           5           10           15

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174/261

ctc acc aat tcc tgg gag atc cga ctt ctc ctc ctt gtg ttc tcc tcc	96
Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser	
20 25 30	
atg ttt tac atg gcc agt atg atg gga aac tct ctc att ttg ctc act	144
Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr	
35 40 45	
gtg act tct gac cct cac ttg cac tcc ccc atg tat ttt ctg tta gcc	192
Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala	
50 55 60	
aac ctc tcc ttc att gac ctg ggt gtt tcc tct gtc act tct ccc aaa	240
Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys	
65 70 75 80	
atg att tat gac ctg ttc aga aag cac gaa gtc atc tcc ttt gga ggc	288
Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly	
85 90 95	
tgc atc gct caa atc ttc ttc atc cac gtc att ggc ggt gtg gag atg	336
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met	
100 105 110	
atg gtg ctg ctc ata gcc atg gcc ttt gac aga tat gtt gcc gta tgt	384
Met Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys	
115 120 125	
aag ccc ctt cac tac ctg acc atc atg cat cca aga atg tgc att ttg	432
Lys Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu	
130 135 140	
att cta gtg gct tcc tgg gcc att ggt ctc att cac tca ttg gtc caa	480
Ile Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln	
145 150 155 160	
ttg tct ttt gta gta aac ttg ccc ttc tgt ggc cct aat gtg ttg gac	528
Leu Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp	
165 170 175	
agc ttt tac tgt gac ata cct cag ctc atc aaa ctt gct tgc aca aat	576
Ser Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn	
180 185 190	
acc tat aaa ctg cag ttc atg gtt act gct aat agt ggg ttc att tcc	624
Thr Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser	
195 200 205	
ttg agt gct ttc ttc ttg ctc atc ctc tct tac atc ttc att ctg gcc	672
Leu Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala	
210 215 220	
act ctt cag aaa cac tcc tca gga ggc tca tcc aag gct gtc tct act	720
Thr Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr	
225 230 235 240	
ctg tca gct cat att act gtt gtg gtt tta ttc ttt ggt cca ctg att	768
Leu Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile	
245 250 255	

[illegible]

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<210> 154
<211> 312
<212> PRT
<213> Homo sapiens
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<400>	154															
Met	Val	Gly	Ala	Asn	His	Ser	Val	Val	Ser	Glu	Phe	Val	Phe	Leu	Gly	
1				5					10					15		
Leu	Thr	Asn	Ser	Trp	Glu	Ile	Arg	Leu	Leu	Leu	Leu	Val	Phe	Ser	Ser	
			20					25					30			
Met	Phe	Tyr	Met	Ala	Ser	Met	Met	Gly	Asn	Ser	Leu	Ile	Leu	Leu	Thr	
		35					40					45				
Val	Thr	Ser	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Phe	Leu	Leu	Ala	
	50					55					60					
Asn	Leu	Ser	Phe	Ile	Asp	Leu	Gly	Val	Ser	Ser	Val	Thr	Ser	Pro	Lys	
65					70					75					80	
Met	Ile	Tyr	Asp	Leu	Phe	Arg	Lys	His	Glu	Val	Ile	Ser	Phe	Gly	Gly	
				85					90					95		
Cys	Ile	Ala	Gln	Ile	Phe	Phe	Ile	His	Val	Ile	Gly	Gly	Val	Glu	Met	
			100					105					110			
Met	Val	Leu	Leu	Ile	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val	Cys	
		115					120					125				
Lys	Pro	Leu	His	Tyr	Leu	Thr	Ile	Met	His	Pro	Arg	Met	Cys	Ile	Leu	
	130					135					140					
Ile	Leu	Val	Ala	Ser	Trp	Ala	Ile	Gly	Leu	Ile	His	Ser	Leu	Val	Gln	
145					150					155					160	
Leu	Ser	Phe	Val	Val	Asn	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Leu	Asp	
				165					170					175		
Ser	Phe	Tyr	Cys	Asp	Ile	Pro	Gln	Leu	Ile	Lys	Leu	Ala	Cys	Thr	Asn	
		180					185					190				
Thr	Tyr	Lys	Leu	Gln	Phe	Met	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile	Ser	
		195					200					205				
Leu	Ser	Ala	Phe	Phe	Leu	Leu	Ile	Leu	Ser	Tyr	Ile	Phe	Ile	Leu	Ala	
	210					215					220					
Thr	Leu	Gln	Lys	His	Ser	Ser	Gly	Gly	Ser	Ser	Lys	Ala	Val	Ser	Thr	
225					230					235					240	
Leu	Ser	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Gly	Pro	Leu	Ile	
				245					250					255		
Phe	Phe	Tyr	Val	Trp	Pro	Ser	Pro	Pro	Thr	His	Leu	Asn	Lys	Phe	Leu	
		260					265					270				
Ala	Ile	Phe	Asp	Ala	Ile	Phe	Thr	Pro	Phe	Leu	Asn	Pro	Val	Ile	Tyr	
	275						280					285				
Thr	Phe	Arg	Asn	Arg	Glu	Met	Lys	Ile	Ala	Ile	Arg	Arg	Val	Phe	Gly	
	290					295					300					

176/261

Gln Phe Met Gly Phe Arg Lys Thr  
305 310

<210> 155  
<211> 951  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(951)

<400> 155  
atg gat gaa gcc aat cac tct gtg gtc tct gag ttt gtg ttc ctg gga 48  
Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly  
1 5 10 15

ctc tct gac tcg cgg aag atc cag ctc ctc ctc ttc ctc ttt ttc tca 96  
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser  
20 25 30

gtg ttc tat gta tca agc ctg atg gga aat ctc ctc att gtg cta act 144  
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr  
35 40 45

gtg acc tct gac cct cgt tta cag tcc ccc atg tac ttc ctg ctg gcc 192  
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala  
50 55 60

aac ctt tcc atc atc aat ttg gta ttt tgt tcc tcc aca gct ccc aag 240  
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys  
65 70 75 80

atg att tat gac ctt ttc agg aag cac aag acc atc tct ttt ggg ggc 288  
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly  
85 90 95

tgt gta gtt cag atc ttc ttt atc cat gca gtt ggg gga act gag atg 336  
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met  
100 105 110

gtg ctg ctc ata gcc atg gct ttt gac cga tat gtg gcc ata tgt aag 384  
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys  
115 120 125

cct ctc cac tac ctg acc atc atg aac cca caa agg tgc att ttg ttt 432  
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe  
130 135 140

tta gtc att tcc tgg att ata gcc act tcc tct atc att ggc ctt atc 480  
Leu Val Ile Ser Trp Ile Ile Ala Thr Ser Ser Ile Ile Gly Leu Ile  
145 150 155 160

cac tca ttg gtc caa tta gtt ttt gtg gta gat tta cct ttt tgt ggt 528  
His Ser Leu Val Gln Leu Val Phe Val Val Asp Leu Pro Phe Cys Gly  
165 170 175

cct aat atc ttt gac agt ttt tac tgt gat ctc cct cgg ctc ctc aga 576  
Pro Asn Ile Phe Asp Ser Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg  
180 185 190

177/261

ctt gcc tgt acc aac acc caa gaa ctg gag ttc atg gtc act gtc aat 624  
 Leu Ala Cys Thr Asn Thr Gln Glu Leu Glu Phe Met Val Thr Val Asn  
                   195                                  200                                  205

agt gga ctc att tct gtg ggc tcc ttt gtc ttg ctg gta att tcc tac 672  
 Ser Gly Leu Ile Ser Val Gly Ser Phe Val Leu Leu Val Ile Ser Tyr  
                   210                                  215                                  220

atc ttc att ctg ttc act gtt tgg aaa cat tct tct ggt ggt cta gcc 720  
 Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly Gly Leu Ala  
                   225                                  230                                  235                                  240

aag gcc ctc tct acc ctg tca gct cat gtc act gtg gtc atc ttg ttc 768  
 Lys Ala Leu Ser Thr Leu Ser Ala His Val Thr Val Val Ile Leu Phe  
                                   245                                  250                                  255

ttt ggg cca ctg atg ttt ttc tac aca tgg cct tct ccc aca tca cac 816  
 Phe Gly Pro Leu Met Phe Phe Tyr Thr Trp Pro Ser Pro Thr Ser His  
                                   260                                  265                                  270

ctg gat aaa tat ctt gct att ttt gat gca ttt att act cct ttt ctg 864  
 Leu Asp Lys Tyr Leu Ala Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu  
                                   275                                  280                                  285

aat cca gtt atc tac aca ttc agg aac aaa gac atg aaa gtg gca atg 912  
 Asn Pro Val Ile Tyr Thr Phe Arg Asn Lys Asp Met Lys Val Ala Met  
                                   290                                  295                                  300

agg aga ctg tgc agt cgt ctt gcg cat ttt aca aag att 951  
 Arg Arg Leu Cys Ser Arg Leu Ala His Phe Thr Lys Ile  
                                   305                                  310                                  315

&lt;210&gt; 156

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 156

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly  
   1                  5                                  10                                  15

Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser  
                   20                                  25                                  30

Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr  
                   35                                  40                                  45

Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala  
                   50                                  55                                  60

Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys  
                   65                                  70                                  75                                  80

Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly  
                                   85                                  90                                  95

Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met  
                                   100                                  105                                  110

Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys  
                                   115                                  120                                  125

Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe  
                   130                                  135                                  140

Leu Val Ile Ser Trp Ile Ile Ala Thr Ser Ser Ile Ile Gly Leu Ile  
                   145                                  150                                  155                                  160

His Ser Leu Val Gln Leu Val Phe Val Val Asp Leu Pro Phe Cys Gly  
                                   165                                  170                                  175

178/261

Pro Asn Ile Phe Asp Ser Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg  
 180 185 190  
 Leu Ala Cys Thr Asn Thr Gln Glu Leu Glu Phe Met Val Thr Val Asn  
 195 200 205  
 Ser Gly Leu Ile Ser Val Gly Ser Phe Val Leu Leu Val Ile Ser Tyr  
 210 215 220  
 Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly Gly Leu Ala  
 225 230 235 240  
 Lys Ala Leu Ser Thr Leu Ser Ala His Val Thr Val Val Ile Leu Phe  
 245 250 255  
 Phe Gly Pro Leu Met Phe Phe Tyr Thr Trp Pro Ser Pro Thr Ser His  
 260 265 270  
 Leu Asp Lys Tyr Leu Ala Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Thr Phe Arg Asn Lys Asp Met Lys Val Ala Met  
 290 295 300  
 Arg Arg Leu Cys Ser Arg Leu Ala His Phe Thr Lys Ile  
 305 310 315

<210> 157  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 157  
 atg gag ata agg aac ttt agt gat cca aca gag ttc gtc ctg gca ggg 48  
 Met Glu Ile Arg Asn Phe Ser Asp Pro Thr Glu Phe Val Leu Ala Gly  
 1 5 10 15  
 ctc cca aat ctc aac agc gca aga gtg gaa tta ttt tct gtg ttt ctt 96  
 Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val Phe Leu  
 20 25 30  
 ctt gtc tat ctc ctg aat ctg aca ggc aat gtg ttg att gtg ggg gtg 144  
 Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val Gly Val  
 35 40 45  
 gta agg gct gat act cga cta cag acc cct atg tac ttc ttt ctg ggt 192  
 Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 aac ctg tcc tgc cta gag ata ctg ctc act tct gtc atc att cca aag 240  
 Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile Pro Lys  
 65 70 75 80  
 atg ctg agc aat ttc ctc tca agg caa cac act att tcc ttt gct gca 288  
 Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe Ala Ala  
 85 90 95  
 tgt atc acc caa ttc tat ttc tac ttc ttt ctc ggg gcc tcc gag ttc 336  
 Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser Glu Phe  
 100 105 110  
 tta ctg ttg gct gtc atg tct gcg gat cgc tac ctg gcc atc tgt cat 384  
 Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile Cys His  
 115 120 125



179/261

cct ctg cgc tac ccc ttg ctc atg agt ggg gct gtg tgc ttt cgt gtg 432  
 Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe Arg Val  
 130 135 140

gcc ttg gcc tgc tgg gtg ggg gga ctc gtc cct gtg ctt ggt ccc aca 480  
 Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly Pro Thr  
 145 150 155 160

gtg gct gtg gcc ttg ctt cct ttc tgt aag cag ggt gct gtg gta cag 528  
 Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val Val Gln  
 165 170 175

cac ttc ttc tgc gac agt ggc cca ctg ctc cgc ctg gct tgc acc aac 576  
 His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys Thr Asn  
 180 185 190

acc aag aag ctg gag gag act gac ttt gtc ctg gcc tcc ctc gtc att 624  
 Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu Val Ile  
 195 200 205

gta tct tcc ttg ctg atc act gct gtg tcc tac ggc ctc att gtg ctg 672  
 Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile Val Leu  
 210 215 220

gca gtc ctg agc atc ccc tct gct tca ggc cgt cag aag gcc ttc tct 720  
 Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala Phe Ser  
 225 230 235 240

acc tgt acc tcc cac ttg ata gtg gtg acc ctc ttc tat gga agt gcc 768  
 Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly Ser Ala  
 245 250 255

att ttt ctc tat gtg cgg cca tcg cag agt ggt tct gtg gac act aac 816  
 Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp Thr Asn  
 260 265 270

tgg gca gtg aca gta ata acg aca ttt gtg aca cca ctg ttg aat cca 864  
 Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu Asn Pro  
 275 280 285

ttc atc tat gcc tta cgt aat gag caa gtc aag gaa gct ttg aag gac 912  
 Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu Lys Asp  
 290 295 300

atg ttt agg aag aag agg gac tgt agc ttt aat 945  
 Met Phe Arg Lys Lys Arg Asp Cys Ser Phe Asn  
 305 310 315

<210> 158  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Glu Ile Arg Asn Phe Ser Asp Pro Thr Glu Phe Val Leu Ala Gly  
 1 5 10 15  
 Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val Phe Leu  
 20 25 30  
 Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val Gly Val  
 35 40 45

180/261

Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe Ala Ala  
 85 90 95  
 Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser Glu Phe  
 100 105 110  
 Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe Arg Val  
 130 135 140  
 Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly Pro Thr  
 145 150 155 160  
 Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val Val Gln  
 165 170 175  
 His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys Thr Asn  
 180 185 190  
 Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu Val Ile  
 195 200 205  
 Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile Val Leu  
 210 215 220  
 Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly Ser Ala  
 245 250 255  
 Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp Thr Asn  
 260 265 270  
 Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu Lys Asp  
 290 295 300  
 Met Phe Arg Lys Lys Arg Asp Cys Ser Phe Asn  
 305 310 315

<210> 159  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 159  
 atg aag ata aag aat cac act cca gta act gag gtc ccc ctg atg gga 48  
 Met Lys Ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly  
 1 5 10 15  
 atc cct cat aca aag ggg atg gaa aat gtg ctt ttt gtc tta ttt ctg 96  
 Ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu  
 20 25 30  
 gcc ttc tac ctc ttc acc ttg ctg ggg aac cta ctc att ctt ctg gcc 144  
 Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Leu Ala  
 35 40 45  
 gtc ctc act ttc tcc aac ctc cac acc ccc atg tat ttc ttc ctg gga 192  
 Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60

181/261

aac ctg tct gtg ttt gac ata ttt ttc cct tca gtg agt tcc ccc aaa	240
Asn Leu Ser Val Phe Asp Ile Phe Phe Pro Ser Val Ser Ser Pro Lys	
65 70 75 80	
atg atg ctc tgc tta gtg gga caa agc tgc acc atc tct ttc cag ggt	288
Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr Ile Ser Phe Gln Gly	
85 90 95	
tgt gcc tcc cag ctc ttc ttt cac cat ttc ctg ggt tgc acc gag tgt	336
Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys	
100 105 110	
ttc ctg tac act gtg atg gcc tat gac cga ttt gca gcc atc tgc cac	384
Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His	
115 120 125	
cct ttg cca tac acg gtc atc atg aaa cgc agg gtg tgt gcc ctc ctg	432
Pro Leu Pro Tyr Thr Val Ile Met Lys Arg Arg Val Cys Ala Leu Leu	
130 135 140	
acg cta ggc acc tgg acg ggg agc tgt ctg cat gca tct gtc ctc aca	480
Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr	
145 150 155 160	
ctc ctc atc ttt aag tta tcc tac tgt ggc ccc aat gaa gtg gac aat	528
Leu Leu Ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn	
165 170 175	
att ttt ttc tgt gat att ccg gtg gtg ctg ccc ctg gcc tgc gca gac	576
Ile Phe Phe Cys Asp Ile Pro Val Leu Pro Leu Ala Cys Ala Asp	
180 185 190	
acc tct cta gca cgg aca gtg agt ttc atc aac gta ggt gtt gtt gcg	624
Thr Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala	
195 200 205	
ctc atg tgt ttt ctt ctt atc ctc acc tct tat gct tgc att gtt atc	672
Leu Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile	
210 215 220	
tct ata ctg aaa atc agt tcc tca gaa ggt agg cgc aga gcc ttc tca	720
Ser Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser	
225 230 235 240	
acc tgc agt gcc cat ctg acg tcc atc ctg ctc ttc tat gga cca ata	768
Thr Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile	
245 250 255	
gtc ctc att tat ctc cga cct gcc tcc agc cct tgg ctg gac tct gtg	816
Val Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val	
260 265 270	
gtt cag gtg ttg aat aat att gtt atc cct tcc ctg aat cct ttg ata	864
Val Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile	
275 280 285	
tat act ttg aga aac aaa ggt gta aag ctg gca ctg aga aag gtg ctc	912
Tyr Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu	
290 295 300	

182/261

att caa gga gta cat aat tgt gga agg  
 ile Gln Gly Val His Asn Cys Gly Arg  
 305 310

939

<210> 160  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Lys ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly  
 1 5 10 15  
 ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu  
 20 25 30  
 Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu ile Leu Leu Ala  
 35 40 45  
 Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Val Phe Asp ile Phe Phe Pro Ser Val Ser Ser Pro Lys  
 65 70 75 80  
 Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr ile Ser Phe Gln Gly  
 85 90 95  
 Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys  
 100 105 110  
 Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala ile Cys His  
 115 120 125  
 Pro Leu Pro Tyr Thr Val ile Met Lys Arg Arg Val Cys Ala Leu Leu  
 130 135 140  
 Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr  
 145 150 155 160  
 Leu Leu ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn  
 165 170 175  
 ile Phe Phe Cys Asp ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp  
 180 185 190  
 Thr Ser Leu Ala Arg Thr Val Ser Phe ile Asn Val Gly Val Val Ala  
 195 200 205  
 Leu Met Cys Phe Leu Leu ile Leu Thr Ser Tyr Ala Cys ile Val ile  
 210 215 220  
 Ser ile Leu Lys ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ala His Leu Thr Ser ile Leu Leu Phe Tyr Gly Pro ile  
 245 250 255  
 Val Leu ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val  
 260 265 270  
 Val Gln Val Leu Asn Asn ile Val ile Pro Ser Leu Asn Pro Leu ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu  
 290 295 300  
 ile Gln Gly Val His Asn Cys Gly Arg  
 305 310

<210> 161  
 <211> 936  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(936)

183/261

<400> 161  
 atg gcc ttg ggg aat cac agc acc atc acc gag ttc ctc ctc ctt ggg 48  
 Met Ala Leu Gly Asn His Ser Thr Ile Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15

ctg tct gcc gac ccc aac atc cgg gct ctg ctc ttt gtg ctg ttc ctg 96  
 Leu Ser Ala Asp Pro Asn Ile Arg Ala Leu Leu Phe Val Leu Phe Leu  
 20 25 30

ggg att tac ctc ctg acc ata atg gaa aac ctg atg ctg ctg ctc atg 144  
 Gly Ile Tyr Leu Leu Thr Ile Met Glu Asn Leu Met Leu Leu Leu Met  
 35 40 45

atc agg gct gat tct tgt ctc cat aag ccc atg tat ttc ttc ctg agt 192  
 Ile Arg Ala Asp Ser Cys Leu His Lys Pro Met Tyr Phe Phe Leu Ser  
 50 55 60

cac ctc tct ttt gtt gat ctc tgc ttc tct tca gtc att gtg ccc aag 240  
 His Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Val Ile Val Pro Lys  
 65 70 75 80

atg ctg gag aac ctc ctg tca cag agg aaa acc att tca gta gag ggc 288  
 Met Leu Glu Asn Leu Leu Ser Gln Arg Lys Thr Ile Ser Val Glu Gly  
 85 90 95

tgc ctg gct cag gtc ttc ttt gtg ttt gtc act gca ggg act gaa gcc 336  
 Cys Leu Ala Gln Val Phe Phe Val Phe Val Thr Ala Gly Thr Glu Ala  
 100 105 110

tgc ctt ctc tca ggg atg gcc tat gac cgc cat gct gcc atc tgc cgc 384  
 Cys Leu Leu Ser Gly Met Ala Tyr Asp Arg His Ala Ala Ile Cys Arg  
 115 120 125

cca cta ctt tat gga cag atc atg ggt aaa cag ctg tat atg cac ctt 432  
 Pro Leu Leu Tyr Gly Gln Ile Met Gly Lys Gln Leu Tyr Met His Leu  
 130 135 140

gtg tgg ggc tca tgg gga ctg ggc ttt ctg gac gca ctc atc aat gtc 480  
 Val Trp Gly Ser Trp Gly Leu Gly Phe Leu Asp Ala Leu Ile Asn Val  
 145 150 155 160

ctc cta gct gta aac atg gtc ttt tgt gaa gcc aaa atc att cac cac 528  
 Leu Leu Ala Val Asn Met Val Phe Cys Glu Ala Lys Ile Ile His His  
 165 170 175

tac agc tat gag atg cca tcc ctc ctc cct ctg tcc tgc tct gat atc 576  
 Tyr Ser Tyr Glu Met Pro Ser Leu Leu Pro Leu Ser Cys Ser Asp Ile  
 180 185 190

tcc aga agc ctc atc gcc ttg ctc tgc tcc act ctc cta cat ggg ctg 624  
 Ser Arg Ser Leu Ile Ala Leu Leu Cys Ser Thr Leu Leu His Gly Leu  
 195 200 205

gga aac ttc ctt ttg gtc ttc tta tcc tac acc cgt ata atc tct acc 672  
 Gly Asn Phe Leu Leu Val Phe Leu Ser Tyr Thr Arg Ile Ile Ser Thr  
 210 215 220

atc cta agc atc agc tct acc tcg ggc aga agc aag gcc ttc tcc acc 720  
 Ile Leu Ser Ile Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240

184/261

tgc tct gcc cac ctc act gca gtg aca ctt tac tat ggc tca ggt ttg	768
Cys Ser Ala His Leu Thr Ala Val Thr Leu Tyr Tyr Gly Ser Gly Leu	
245 250 255	
ctc cgc cat ctc atg cca aac tca ggt tcc ccc ata gag ttg atc ttc	816
Leu Arg His Leu Met Pro Asn Ser Gly Ser Pro Ile Glu Leu Ile Phe	
260 265 270	
tct gtg cag tat act gta gtc act ccc atg ctg aat tcc ctc atc tat	864
Ser Val Gln Tyr Thr Val Val Thr Pro Met Leu Asn Ser Leu Ile Tyr	
275 280 285	
agc ctg aaa aat aag gaa gtg aag gta gct ctg aaa aga act ttg gaa	912
Ser Leu Lys Asn Lys Glu Val Lys Val Ala Leu Lys Arg Thr Leu Glu	
290 295 300	
aaa tat ttg caa tat acc aga cgt	936
Lys Tyr Leu Gln Tyr Thr Arg Arg	
305 310	

&lt;210&gt; 162

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

Met Ala Leu Gly Asn His Ser Thr Ile Thr Glu Phe Leu Leu Leu Gly	
1 5 10 15	
Leu Ser Ala Asp Pro Asn Ile Arg Ala Leu Leu Phe Val Leu Phe Leu	
20 25 30	
Gly Ile Tyr Leu Leu Thr Ile Met Glu Asn Leu Met Leu Leu Leu Met	
35 40 45	
Ile Arg Ala Asp Ser Cys Leu His Lys Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
His Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Val Ile Val Pro Lys	
65 70 75 80	
Met Leu Glu Asn Leu Leu Ser Gln Arg Lys Thr Ile Ser Val Glu Gly	
85 90 95	
Cys Leu Ala Gln Val Phe Phe Val Phe Val Thr Ala Gly Thr Glu Ala	
100 105 110	
Cys Leu Leu Tyr Gly Met Ala Tyr Asp Arg His Ala Ala Ile Cys Arg	
115 120 125	
Pro Leu Leu Tyr Gly Gln Ile Met Gly Lys Gln Leu Tyr Met His Leu	
130 135 140	
Val Trp Gly Ser Trp Gly Leu Gly Phe Leu Asp Ala Leu Ile Asn Val	
145 150 155 160	
Leu Leu Ala Val Asn Met Val Phe Cys Glu Ala Lys Ile Ile His His	
165 170 175	
Tyr Ser Tyr Glu Met Pro Ser Leu Leu Pro Leu Ser Cys Ser Asp Ile	
180 185 190	
Ser Arg Ser Leu Ile Ala Leu Leu Cys Ser Thr Leu Leu His Gly Leu	
195 200 205	
Gly Asn Phe Leu Leu Val Phe Leu Ser Tyr Thr Arg Ile Ile Ser Thr	
210 215 220	
Ile Leu Ser Ile Ser Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr	
225 230 235 240	
Cys Ser Ala His Leu Thr Ala Val Thr Leu Tyr Tyr Gly Ser Gly Leu	
245 250 255	
Leu Arg His Leu Met Pro Asn Ser Gly Ser Pro Ile Glu Leu Ile Phe	
260 265 270	

185/261

Ser Val Gln Tyr Thr Val Val Thr Pro Met Leu Asn Ser Leu Ile Tyr  
 275 280 285  
 Ser Leu Lys Asn Lys Glu Val Lys Val Ala Leu Lys Arg Thr Leu Glu  
 290 295 300  
 Lys Tyr Leu Gln Tyr Thr Arg Arg  
 305 310

<210> 163  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 163  
 act tct cag aat caa aca gca agc act gat ttc acc ctc acg gga ctc 48  
 Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp Phe Thr Leu Thr Gly Leu  
 1 5 10 15  
 ttt gct gag agc aag cat gct gcc ctc ctc tac acc gtg acc ttc ctt 96  
 Phe Ala Glu Ser Lys His Ala Ala Leu Leu Tyr Thr Val Thr Phe Leu  
 20 25 30  
 ctt ttc ttg atg gcc ctc act ggg aat gcc ctc ctc atc ctc ctc atc 144  
 Leu Phe Leu Met Ala Leu Thr Gly Asn Ala Leu Leu Ile Leu Leu Ile  
 35 40 45  
 cac tca gag ccc cgc ctc cac acc ccc atg tac ttc ttc atc agc cag 192  
 His Ser Glu Pro Arg Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln  
 50 55 60  
 ctc gcg ctc atg gat ctc atg tac cta tgc gtg act gtg ccc aag atg 240  
 Leu Ala Leu Met Asp Leu Met Tyr Leu Cys Val Thr Val Pro Lys Met  
 65 70 75 80  
 ctt gtg ggc cag gtc act gga gat gat acc att tcc ccg tca ggc tgt 288  
 Leu Val Gly Gln Val Thr Gly Asp Asp Thr Ile Ser Pro Ser Gly Cys  
 85 90 95  
 ggg atc cag atg ttc ttc cac ctg acc ctg gct gga gct gag gtt ttc 336  
 Gly Ile Gln Met Phe Phe His Leu Thr Leu Ala Gly Ala Glu Val Phe  
 100 105 110  
 ctc ctg gct gcc atg gcc tat gac cga tat gct gct gtt tgc aga cct 384  
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro  
 115 120 125  
 ctc cat tac cca ctg ctg atg aac cag agg gtg tgc cag ctc ctg gtg 432  
 Leu His Tyr Pro Leu Leu Met Asn Gln Arg Val Cys Gln Leu Leu Val  
 130 135 140  
 tca gcc tgc tgg gtt ttg gga atg gtt gat ggt ttg ttg ctc acc ccc 480  
 Ser Ala Cys Trp Val Leu Gly Met Val Asp Gly Leu Leu Leu Thr Pro  
 145 150 155 160  
 att acc atg agc ttc ccc ttt tgc caa tcc tgg gag att cat cat ttc 528  
 Ile Thr Met Ser Phe Pro Phe Cys Gln Ser Trp Glu Ile His His Phe  
 165 170 175

186/261

ttc tgt gaa gtc cct gct gta acg atc ctg tcc tgc tca gac acc tca 576  
 Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser Cys Ser Asp Thr Ser  
                   180                  185                  190

ctc tat gag acc ctc atg tac cta tgc tgt gtc ctc atg ctc ctc atc 624  
 Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile  
                   195                  200                  205

cct gtg acg atc att tca agc tcc tat tta ctc atc ctc ctc acc gtc 672  
 Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Val  
                   210                  215                  220

cac agg atg aac tca gca gag ggc cgg aaa aag gcc ttt gcc acc tgc 720  
 His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225                  230                  235                  240

tcc tcc cac ctg act gtg gtc atc ctc ttc tat ggg gct gcc gtc tac 768  
 Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Val Tyr  
                   245                  250                  255

acc tac atg ctc ccc agc tcc tac cac acc cct gag aag gac atg atg 816  
 Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met  
                   260                  265                  270

gta tct gtc ttc tat acc atc ctc act ccg gtg ctg aac cct tta atc 864  
 Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Leu Asn Pro Leu Ile  
                   275                  280                  285

tat agt ctt agg aat aag gat gtc atg ggg gct ctg aag aaa atg tta 912  
 Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu  
                   290                  295                  300

act gtg aga ttc act cac tca gag tgg 939  
 Thr Val Arg Phe Thr His Ser Glu Trp  
 305                  310

&lt;210&gt; 164

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp Phe Thr Leu Thr Gly Leu  
 1                  5                  10                  15  
 Phe Ala Glu Ser Lys His Ala Ala Leu Leu Tyr Thr Val Thr Phe Leu  
                   20                  25                  30  
 Leu Phe Leu Met Ala Leu Thr Gly Asn Ala Leu Leu Ile Leu Leu Ile  
                   35                  40                  45  
 His Ser Glu Pro Arg Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln  
                   50                  55                  60  
 Leu Ala Leu Met Asp Leu Met Tyr Leu Cys Val Thr Val Pro Lys Met  
 65                  70                  75                  80  
 Leu Val Gly Gln Val Thr Gly Asp Asp Thr Ile Ser Pro Ser Gly Cys  
                   85                  90                  95  
 Gly Ile Gln Met Phe Phe His Leu Thr Leu Ala Gly Ala Glu Val Phe  
                   100                  105                  110  
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro  
                   115                  120                  125  
 Leu His Tyr Pro Leu Leu Met Asn Gln Arg Val Cys Gln Leu Leu Val  
                   130                  135                  140



187/261

Ser Ala Cys Trp Val Leu Gly Met Val Asp Gly Leu Leu Leu Thr Pro  
 145 150 155 160  
 Ile Thr Met Ser Phe Pro Phe Cys Gln Ser Trp Glu Ile His His Phe  
 165 170 175  
 Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser Cys Ser Asp Thr Ser  
 180 185 190  
 Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile  
 195 200 205  
 Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Val  
 210 215 220  
 His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Val Tyr  
 245 250 255  
 Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met  
 260 265 270  
 Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu  
 290 295 300  
 Thr Val Arg Phe Thr His Ser Glu Trp  
 305 310

<210> 165  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 165  
 atg gag atg aga aat act acc cca gac ttt att ctc ctg gga ctc ttt 48  
 Met Glu Met Arg Asn Thr Thr Pro Asp Phe Ile Leu Leu Gly Leu Phe  
 1 5 10 15  
 aac cac acc aga gcc cac caa gtc ctc ttc atg atg gtt ctg agt atc 96  
 Asn His Thr Arg Ala His Gln Val Leu Phe Met Met Val Leu Ser Ile  
 20 25 30  
 gtt ttg acc tcc ctg ttt ggc aat tcc ctc atg att ctc ctg att cac 144  
 Val Leu Thr Ser Leu Phe Gly Asn Ser Leu Met Ile Leu Leu Ile His  
 35 40 45  
 cgg gac acc ggc cgg ctc cac acg ccc atg tac ttc ctc ctg agc caa 192  
 Arg Asp Thr Gly Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50 55 60  
 ctc tcc ctc atg gac gtg atg ctg gtt tcc acc act gtg ccc aaa atg 240  
 Leu Ser Leu Met Asp Val Met Leu Val Ser Thr Thr Val Pro Lys Met  
 65 70 75 80  
 gcg gct gac tac ttg acc gga aat aag gcc atc tcc cgc gct ggc tgt 288  
 Ala Ala Asp Tyr Leu Thr Gly Asn Lys Ala Ile Ser Arg Ala Gly Cys  
 85 90 95  
 ggt gtg cag atc ttc ttc ctc ccc aca ctg ggt ggt gga gag tgc ttc 336  
 Gly Val Gln Ile Phe Phe Leu Pro Thr Leu Gly Gly Gly Glu Cys Phe  
 100 105 110

188/261

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ctc tta gca gcc atg gcc tat gac cgc tat gcg gct gtc tgc cac cca 384
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys His Pro
115 120 125

ctc cga tat ccc act ctc atg agc tgg cag ctg tgc ctg agg atg acc 432
Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu Cys Leu Arg Met Thr
130 135 140

atg tgc tcc tgg ctc ctg ggt gca gct gac ggg ctc ctg cag gct gtt 480
Met Ser Ser Trp Leu Leu Gly Ala Ala Asp Gly Leu Leu Gln Ala Val
145 150 155 160

gct acc ctg agc ttc cca tat tgc ggt gca cac gag atc gat cac ttc 528
Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His Glu Ile Asp His Phe
165 170 175

ttc tgc gag gcc ccc gtg ctg gtg cgt ttg gct tgt gct gac act tca 576
Phe Cys Glu Ala Pro Val Leu Val Arg Leu Ala Cys Ala Asp Thr Ser
180 185 190

gtc ttc gaa aac gcc atg tac atc tgc tgt gtg tta atg ctc ctg gtc 624
Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val Leu Met Leu Leu Val
195 200 205

ccc ttt tcc ctc atc ctg tcc tcc tat ggt ctc atc ctc gct gct gtt 672
Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu Ile Leu Ala Ala Val
210 215 220

ctg cac atg cgc tct aca gaa gcc cgc aag aag gcc ttc gcc acc tgc 720
Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys Ala Phe Ala Thr Cys
225 230 235 240

tct tca cat gtg gct gtg gtg gga ctc ttt tat gga gct gcc att ttt 768
Ser Ser His Val Ala Val Val Gly Leu Phe Tyr Gly Ala Ala Ile Phe
245 250 255

acc tat atg aga ccc aaa tcc cac agg tcc act aac cac gac aag gtt 816
Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr Asn His Asp Lys Val
260 265 270

gtg tca gcc ttc tat agt atg ttc acc cct tta cta aac ccc ctc atc 864
Val Ser Ala Phe Tyr Ser Met Phe Thr Pro Leu Leu Asn Pro Leu Ile
275 280 285

tac agt gtg agg aac agt gag gtc aag gaa gcc ctg aaa cgg tgg ctg 912
Tyr Ser Val Arg Asn Ser Glu Val Lys Glu Ala Leu Lys Arg Trp Leu
290 295 300

ggg aca tgt gta aac ctg aaa cac cag 939
Gly Thr Cys Val Asn Leu Lys His Gln
305 310

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&lt;210&gt; 166

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 166

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Met Glu Met Arg Asn Thr Thr Pro Asp Phe Ile Leu Leu Gly Leu Phe
1 5 10 15

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189/261

Asn His Thr Arg Ala His Gln Val Leu Phe Met Met Val Leu Ser Ile  
                   20                  25                  30  
 Val Leu Thr Ser Leu Phe Gly Asn Ser Leu Met Ile Leu Leu Ile His  
                   35                  40                  45  
 Arg Asp Thr Gly Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
                   50                  55                  60  
 Leu Ser Leu Met Asp Val Met Leu Val Ser Thr Thr Val Pro Lys Met  
                   65                  70                  75                  80  
 Ala Ala Asp Tyr Leu Thr Gly Asn Lys Ala Ile Ser Arg Ala Gly Cys  
                   85                  90                  95  
 Gly Val Gln Ile Phe Phe Leu Pro Thr Leu Gly Gly Gly Glu Cys Phe  
                   100                  105                  110  
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys His Pro  
                   115                  120                  125  
 Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu Cys Leu Arg Met Thr  
                   130                  135                  140  
 Met Ser Ser Trp Leu Leu Gly Ala Ala Asp Gly Leu Leu Gln Ala Val  
                   145                  150                  155                  160  
 Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His Glu Ile Asp His Phe  
                   165                  170                  175  
 Phe Cys Glu Ala Pro Val Leu Val Arg Leu Ala Cys Ala Asp Thr Ser  
                   180                  185                  190  
 Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val Leu Met Leu Leu Val  
                   195                  200                  205  
 Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu Ile Leu Ala Ala Val  
                   210                  215                  220  
 Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys Ala Phe Ala Thr Cys  
                   225                  230                  235                  240  
 Ser Ser His Val Ala Val Val Gly Leu Phe Tyr Gly Ala Ala Ile Phe  
                   245                  250                  255  
 Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr Asn His Asp Lys Val  
                   260                  265                  270  
 Val Ser Ala Phe Tyr Ser Met Phe Thr Pro Leu Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Val Arg Asn Ser Glu Val Lys Glu Ala Leu Lys Arg Trp Leu  
                   290                  295                  300  
 Gly Thr Cys Val Asn Leu Lys His Gln  
                   305                  310

&lt;210&gt; 167

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(930)

&lt;400&gt; 167

atg gag aat agg aat aac gtg aca gag ttt gtt tta cta ggg ctt aca 48  
 Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr  
   1                  5                  10                  15

gag aat cca aag atg cag aaa atc ata ttt gtt gtg ttt ttt ttt gtc 96  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val  
                   20                  25                  30

atc tat atc atc act gtg gtg gga aat gcg ctc att gtg gtc acc atc 144  
 Ile Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile  
                   35                  40                  45

190/261

act gcc agc cca tca ctg ggg tcc ccc atg tac ctt ttc ctg gcc tat	192
Thr Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr	
50 55 60	
ctc tcc ttt ata gat gcc tgc tat tct tct gtc aat acc cct aag ctg	240
Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu	
65 70 75 80	
atc aca gat tca ctc tat gga aag aac acc atc cta ttc aat gga tgc	288
Ile Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys	
85 90 95	
atg act caa gtc ttt gga gaa cat ttc ttc gga ggt gca gag ggt atc	336
Met Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile	
100 105 110	
cta ctt act gtg atg gcc tat gac cgc tat gtg gcc atc tgc aag ccc	384
Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro	
115 120 125	
ttg cac tat atg act atc atg aac cag tgt gtg tat gcc ctg cta atg	432
Leu His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met	
130 135 140	
gga gtg gtg tgg atg gga ggc ttt ctt cat gca acc ata cag atc ctc	480
Gly Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu	
145 150 155 160	
ttc atc ttc caa tta cct ttc tgt ggt cct aat gtc ata gat cac ttt	528
Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe	
165 170 175	
atg tgt gat ctg aac cct ttg ctc aac ctc gcc tgc act gac acc cat	576
Met Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His	
180 185 190	
atg ctg gga ctc ttc att gct gcc aac agt gga ttc atc tgc ttg tta	624
Met Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu	
195 200 205	
aac ttt gtc ctc ctg ctg gtc tcc tat gtg gtc atc ttg cgc tcc cta	672
Asn Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu	
210 215 220	
agg act cac agc ttg gag gca agg cac aaa gcc ctc tcc acc tgt gtc	720
Arg Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val	
225 230 235 240	
tcc cac atc aca gtt gtc atc tta ttc ttt gtg ccc tgc ata ttt gtg	768
Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val	
245 250 255	
tac atg aga cct gca gct act tta cct att gat aaa gca gtt gct ata	816
Tyr Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile	
260 265 270	
ttc tac act atg ata act cct atg tta aac ccc tta atc tat acc ttg	864
Phe Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Tyr Thr Leu	
275 280 285	

191/261

agg aat gcc cag atg aaa aat gcc atc agg aaa ttg tgt agt aga aag 912  
 Arg Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys  
 290 295 300

gac att tca ggt aac aaa 930  
 Asp Ile Ser Gly Asn Lys  
 305 310

<210> 168  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

<400> 168  
 Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr  
 1 5 10 15  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Phe Val  
 20 25 30  
 Ile Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile  
 35 40 45  
 Thr Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr  
 50 55 60  
 Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu  
 65 70 75 80  
 Ile Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys  
 85 90 95  
 Met Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile  
 100 105 110  
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro  
 115 120 125  
 Leu His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met  
 130 135 140  
 Gly Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu  
 145 150 155 160  
 Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe  
 165 170 175  
 Met Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His  
 180 185 190  
 Met Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu  
 195 200 205  
 Asn Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu  
 210 215 220  
 Arg Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val  
 225 230 235 240  
 Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val  
 245 250 255  
 Tyr Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile  
 260 265 270  
 Phe Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu  
 275 280 285  
 Arg Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys  
 290 295 300  
 Asp Ile Ser Gly Asn Lys  
 305 310

<210> 169  
 <211> 933  
 <212> DNA  
 <213> Homo sapiens

192/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(933)

&lt;400&gt; 169

atg aag aga gcc aat cac aca gag tta aga gag ttt gtt ttc caa ggt	48
Met Lys Arg Ala Asn His Thr Glu Leu Arg Glu Phe Val Phe Gln Gly	
1 5 10 15	
ttc tcc aat ttt cca gaa cat cag ctc aca ttt ttt gtg gtc ttt ctc	96
Phe Ser Asn Phe Pro Glu His Gln Leu Thr Phe Phe Val Val Phe Leu	
20 25 30	
gcc ctc tac aca ttc cta act ctg gct ggc aat ttc atc att ctg gcc	144
Ala Leu Tyr Thr Phe Leu Thr Leu Ala Gly Asn Phe Ile Ile Leu Ala	
35 40 45	
ata atc tat gtt gac cat cac ctc cat act cct atg tac ttc ttt tta	192
Ile Ile Tyr Val Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu	
50 55 60	
agt gtg cta tcc act tca gag act ttc tat tcc ctg gtc att atc cca	240
Ser Val Leu Ser Thr Ser Glu Thr Phe Tyr Ser Leu Val Ile Ile Pro	
65 70 75 80	
cgc atg ctt tcc agc ctt gta ggc ctg agc caa tcc att tcc ctg gag	288
Arg Met Leu Ser Ser Leu Val Gly Leu Ser Gln Ser Ile Ser Leu Glu	
85 90 95	
ggc tgt ggg act cag atc ttt ttt ttt ctt ggc ttt gcc atc acc aac	336
Gly Cys Gly Thr Gln Ile Phe Phe Phe Leu Gly Phe Ala Ile Thr Asn	
100 105 110	
tgc ctc ctg cta gca gta atg gaa tat gat cac tac gtg gcc gtc tgc	384
Cys Leu Leu Leu Ala Val Met Glu Tyr Asp His Tyr Val Ala Val Cys	
115 120 125	
aac cca ctt cga tac tca gtc atc atg aat tgg agg gtg tgt gct ata	432
Asn Pro Leu Arg Tyr Ser Val Ile Met Asn Trp Arg Val Cys Ala Ile	
130 135 140	
ctg gca tca tca gtc tgt gcc aca ggg ttc tca ctc tca ctg gtt cag	480
Leu Ala Ser Ser Val Cys Ala Thr Gly Phe Ser Leu Ser Leu Val Gln	
145 150 155 160	
act gtg gcc att ttc agg ttg ctc ttt tgc acc cca ctg att gag cat	528
Thr Val Ala Ile Phe Arg Leu Leu Phe Cys Thr Pro Leu Ile Glu His	
165 170 175	
ttc ttc tgt gat gtt cag cct gtg ttg gac ctg gcc tgg gct acc cca	576
Phe Phe Cys Asp Val Gln Pro Val Leu Asp Leu Ala Trp Ala Thr Pro	
180 185 190	
atg atc aat gat att ctg acc tta att atg agc ctc ctt gcc atc aca	624
Met Ile Asn Asp Ile Leu Thr Leu Ile Met Ser Leu Leu Ala Ile Thr	
195 200 205	
gcc cca gcc atc ttc ctc ttc atc tct tat gtc ctt att att tcc acc	672
Ala Pro Ala Ile Phe Leu Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr	
210 215 220	

193/261

att ctc aag atc acc tca gct gaa ggc ggg aag aag acc ttt gcc acc 720  
 Ile Leu Lys Ile Thr Ser Ala Glu Gly Gly Lys Lys Thr Phe Ala Thr  
 225 230 235 240

tat gca tcc cac ctc act gtg gtc att atc cac tat ggc tgt gcc tcc 768  
 Tyr Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
 245 250 255

att gcc tac ttc aag ccc aat ttg gag aat acc aaa gat cag gat cag 816  
 Ile Ala Tyr Phe Lys Pro Asn Leu Glu Asn Thr Lys Asp Gln Asp Gln  
 260 265 270

tta atc tca gtg acc tac act gtc ata aca cct tta cta aac cct gtt 864  
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val  
 275 280 285

gtg tat ggt ctg aga aat aaa gaa gtc cag gat gct ctg cag aga gtg 912  
 Val Tyr Gly Leu Arg Asn Lys Glu Val Gln Asp Ala Leu Gln Arg Val  
 290 295 300

ctg ggt agg aaa ttc ttc tcc 933  
 Leu Gly Arg Lys Phe Phe Ser  
 305 310

<210> 170  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Lys Arg Ala Asn His Thr Glu Leu Arg Glu Phe Val Phe Gln Gly  
 1 5 10 15  
 Phe Ser Asn Phe Pro Glu His Gln Leu Thr Phe Phe Val Val Phe Leu  
 20 25 30  
 Ala Leu Tyr Thr Phe Leu Thr Leu Ala Gly Asn Phe Ile Ile Leu Ala  
 35 40 45  
 Ile Ile Tyr Val Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Val Leu Ser Thr Ser Glu Thr Phe Tyr Ser Leu Val Ile Ile Pro  
 65 70 75 80  
 Arg Met Leu Ser Ser Leu Val Gly Leu Ser Gln Ser Ile Ser Leu Glu  
 85 90 95  
 Gly Cys Gly Thr Gln Ile Phe Phe Phe Leu Gly Phe Ala Ile Thr Asn  
 100 105 110  
 Cys Leu Leu Leu Ala Val Met Glu Tyr Asp His Tyr Val Ala Val Cys  
 115 120 125  
 Asn Pro Leu Arg Tyr Ser Val Ile Met Asn Trp Arg Val Cys Ala Ile  
 130 135 140  
 Leu Ala Ser Ser Val Cys Ala Thr Gly Phe Ser Leu Ser Leu Val Gln  
 145 150 155 160  
 Thr Val Ala Ile Phe Arg Leu Leu Phe Cys Thr Pro Leu Ile Glu His  
 165 170 175  
 Phe Phe Cys Asp Val Gln Pro Val Leu Asp Leu Ala Trp Ala Thr Pro  
 180 185 190  
 Met Ile Asn Asp Ile Leu Thr Leu Ile Met Ser Leu Leu Ala Ile Thr  
 195 200 205  
 Ala Pro Ala Ile Phe Leu Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Thr Ser Ala Glu Gly Gly Lys Lys Thr Phe Ala Thr  
 225 230 235 240

194/261

Tyr Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
                           245                          250                          255  
 Ile Ala Tyr Phe Lys Pro Asn Leu Glu Asn Thr Lys Asp Gln Asp Gln  
                           260                          265                          270  
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val  
                           275                          280                          285  
 Val Tyr Gly Leu Arg Asn Lys Glu Val Gln Asp Ala Leu Gln Arg Val  
                           290                          295                          300  
 Leu Gly Arg Lys Phe Phe Ser  
 305                          310

<210> 171  
 <211> 927  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(927)

<400> 171  
 atg cag caa aat aac agt gtg act gaa ttc ata ctg tta gga tta aca 48  
 Met Gln Gln Asn Asn Ser Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
   1                          5                          10                          15  
  
 cag gat ccc ttg agg cag aaa ata gtg ttt gta atc ttc tta att ttc 96  
 Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile Phe  
                           20                          25                          30  
  
 tat atg gga act gtg gtg ggg aat atg ctc att att gtg acc atc aag 144  
 Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile Lys  
                           35                          40                          45  
  
 tcc agc cgg aca cta gga agc ccc atg tac ttc ttt cta ttt tat ttg 192  
 Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr Leu  
                           50                          55                          60  
  
 tcc ttt gca gat tct tgc ttt tca act tcc aca gcc cct aga tta att 240  
 Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu Ile  
   65                          70                          75                          80  
  
 gtg gat gct ctc tct gaa aag aaa att ata acc tac aat gag tgc atg 288  
 Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys Met  
                           85                          90                          95  
  
 aca caa gtc ttt gca cta cat tta ttt ggc tgc atg gag atc ttt gtc 336  
 Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe Val  
                           100                          105                          110  
  
 ctc att ctc atg gct gtt gat cgc tat gtg gcc atc tgt aag ccc ttg 384  
 Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
                           115                          120                          125  
  
 cgt tac cca acc atc atg agc cag cag gtc tgc atc atc ctg att gtt 432  
 Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile Val  
                           130                          135                          140  
  
 ctt gcc tgg ata ggg tct tta ata cac tct aca gct cag att atc ctg 480  
 Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile Leu  
  145                          150                          155                          160



195/261

gcc tta aga ttg cct ttc tgt gga ccc tat ttg att gat cat tat tgc 528  
 Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr Cys  
 165 170 175

tgt gat ttg cag ccc ttg ttg aaa ctt gcc tgc atg gac act tac atg 576  
 Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr Met  
 180 185 190

atc aac ctg ctg ttg gtg tct aac agt ggg gca att tgc tca agt agt 624  
 Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser Ser  
 195 200 205

ttc atg att ttg ata att tca tat att gtc atc ttg cat tca ctg aga 672  
 Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu Arg  
 210 215 220

aac cac agt gcc aaa ggg aag aaa aag gct ctc tcc gct tgc acg tct 720  
 Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr Ser  
 225 230 235 240

cac ata att gta gtc atc tta ttc ttt ggc cca tgt ata ttc ata tat 768  
 His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile Tyr  
 245 250 255

aca cgc ccc ccg acc act ttc ccc atg gac aag atg gtg gca gta ttt 816  
 Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val Phe  
 260 265 270

tat act att gga cca ccc ttt ctc aat cca ctc atc tac aca ctg agg 864  
 Tyr Thr Ile Gly Pro Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285

aat gca gaa gtg aaa aat gcc atg aga aag tta tgg cat ggc aaa att 912  
 Asn Ala Glu Val Lys Asn Ala Met Arg Lys Leu Trp His Gly Lys Ile  
 290 295 300

att tca gaa aac aaa 927  
 Ile Ser Glu Asn Lys  
 305

&lt;210&gt; 172

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

Met Gln Gln Asn Asn Ser Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15

Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile Phe  
 20 25 30

Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile Lys  
 35 40 45

Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr Leu  
 50 55 60

Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu Ile  
 65 70 75 80

Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys Met  
 85 90 95

Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe Val  
 100 105 110

196/261

Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile Val  
 130 135 140  
 Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile Leu  
 145 150 155 160  
 Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr Cys  
 165 170 175  
 Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr Met  
 180 185 190  
 Ile Asn Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser Ser  
 195 200 205  
 Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu Arg  
 210 215 220  
 Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr Ser  
 225 230 235 240  
 His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile Tyr  
 245 250 255  
 Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val Phe  
 260 265 270  
 Tyr Thr Ile Gly Pro Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Asn Ala Met Arg Lys Leu Trp His Gly Lys Ile  
 290 295 300  
 Ile Ser Glu Asn Lys  
 305

<210> 173  
 <211> 912  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)... (912)

<400> 173  
 gaa ttc ctc ctc ctg gga atc tca gag gat cca gaa ctg cag ccc gtc 48  
 Glu Phe Leu Leu Leu Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val  
 1 5 10 15  
 ctc gct ggg ctg acc ctg tcc atg tac ctg gtc acg gtg ctg agg aac 96  
 Leu Ala Gly Leu Thr Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn  
 20 25 30  
 ctg ctc atc atc ctg gct gtc agc tct gac tcc cac ctc cac acc tcc 144  
 Leu Leu Ile Ile Leu Ala Val Ser Ser Asp Ser His Leu His Thr Ser  
 35 40 45  
 atg tac ttc gtc ctc tcc aac ctg cgc tgg gtt gac atc ggt ttc acc 192  
 Met Tyr Phe Val Leu Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr  
 50 55 60  
 tcg gcc acg gtt ccc aag atg att gtg gac atg cag tcg cat agc aga 240  
 Ser Ala Thr Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg  
 65 70 75 80  
 gtc atc tct tat gcg ggc tgc ctg aca cag atg tct ttc ttg gtc ttt 288  
 Val Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe  
 85 90 95

197/261

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ttt gca tgt ata gaa gac atg ctc ctg act gtg atg tcc tat gac caa 336
Phe Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln
100 105 110

ttt ttg gcc atc tgt cac ccc ctg cac tac cca gtc atc gtg aat cct 384
Phe Leu Ala Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro
115 120 125

cac ttc tgt gtc ttc tta gtt ttg gtg tcc ttt ttc ctt agc ctg ttg 432
His Phe Cys Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu
130 135 140

gat tcc cag ctg cat aga tgg att gtg tta caa ttc acc ttc ttc aag 480
Asp Ser Gln Leu His Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys
145 150 155 160

aat gtg gaa atc tct aat ttt gtc tgt gag cca tct caa ctt ctc aac 528
Asn Val Glu Ile Ser Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn
165 170 175

ctt gcc tgt tct gac agc gtc atc aat atc ata ttc ata tat tta gat 576
Leu Ala Cys Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp
180 185 190

agt act atg ttt ggt ttt ctt ccc att tca ggg atc ctt ttg tct tac 624
Ser Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr
195 200 205

tat aaa att gtc ccc tcc att cta agg atg tca ttg tca gat gtg aag 672
Tyr Lys Ile Val Pro Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys
210 215 220

tat aaa gcc ttc tcc acc tgt ggc tct cac ctg gca gtt ttt tgc tta 720
Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu
225 230 235 240

ttt tac gga gca ggc att ggc gtg tac ctg act tca gct gtg tca cca 768
Phe Tyr Gly Ala Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro
245 250 255

cct tcc ggc aat ggt gtg gtg gct tca gtg atg tac act gtg gtc acc 816
Pro Ser Gly Asn Gly Val Val Ala Ser Val Met Tyr Thr Val Val Thr
260 265 270

ccc atg ctg aac cct ttc atc tac agc ctg aga aac agg gac att caa 864
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln
275 280 285

agt gcc ccg tgg agg ctg cgc agc aca aca gtt gaa tct cat gat ctc 912
Ser Ala Pro Trp Arg Leu Arg Ser Thr Thr Val Glu Ser His Asp Leu
290 295 300

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<210> 174  
 <211> 304  
 <212> PRT  
 <213> Homo sapiens

<400> 174  
 Glu Phe Leu Leu Leu Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val  
 1 5 10 15

198/261

Leu Ala Gly Leu Thr Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn  
                   20                  25                  30  
 Leu Leu Ile Ile Leu Ala Val Ser Ser Asp Ser His Leu His Thr Ser  
                   35                  40                  45  
 Met Tyr Phe Val Leu Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr  
                   50                  55                  60  
 Ser Ala Thr Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg  
                   65                  70                  75                  80  
 Val Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe  
                   85                  90                  95  
 Phe Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln  
                   100                  105                  110  
 Phe Leu Ala Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro  
                   115                  120                  125  
 His Phe Cys Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu  
                   130                  135                  140  
 Asp Ser Gln Leu His Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys  
                   145                  150                  155                  160  
 Asn Val Glu Ile Ser Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn  
                   165                  170                  175  
 Leu Ala Cys Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp  
                   180                  185                  190  
 Ser Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr  
                   195                  200                  205  
 Tyr Lys Ile Val Pro Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys  
                   210                  215                  220  
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu  
                   225                  230                  235                  240  
 Phe Tyr Gly Ala Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro  
                   245                  250                  255  
 Pro Ser Gly Asn Gly Val Val Ser Val Met Tyr Thr Val Val Thr  
                   260                  265                  270  
 Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln  
                   275                  280                  285  
 Ser Ala Pro Trp Arg Leu Arg Ser Thr Thr Val Glu Ser His Asp Leu  
                   290                  295                  300

<210> 175  
 <211> 921  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (921)

<400> 175  
 atg gag cca agg aaa aat gtg act gac ttt gtc ctc ttg ggc ttc aca 48  
 Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr  
   1                  5                  10                  15  
  
 cag aat cca aag gag cag aaa gta ctt ttt gtt atg ttc ttg ctc ttc 96  
 Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe  
                   20                  25                  30  
  
 tac att ttg acc atg gtg ggc aac ctg ctc att gta gtg acc gta act 144  
 Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr  
                   35                  40                  45  
  
 gtc agt gag acc ctg ggc tca cca atg tcc ttc ttt ctt gct ggc tta 192

199/261

Val	Ser	Glu	Thr	Leu	Gly	Ser	Pro	Met	Ser	Phe	Phe	Leu	Ala	Gly	Leu		
50						55					60						
aca	ttt	ata	gat	atc	att	tat	tct	tca	tcc	att	tcc	ccc	aga	ttg	att	240	
Thr	Phe	Ile	Asp	Ile	Ile	Tyr	Ser	Ser	Ser	Ile	Ser	Pro	Arg	Leu	Ile		
65					70					75					80		
tca	gac	ttg	ttc	ttt	ggg	aat	aat	tcc	ata	tcc	ttc	caa	tct	ttc	atg	288	
Ser	Asp	Leu	Phe	Phe	Gly	Asn	Asn	Ser	Ile	Ser	Phe	Gln	Ser	Phe	Met		
				85				90						95			
gcc	cag	ctc	ttt	atc	gag	cac	ctt	ttt	ggg	ggg	tca	gag	gtc	ttt	ctc	336	
Ala	Gln	Leu	Phe	Ile	Glu	His	Leu	Phe	Gly	Gly	Ser	Glu	Val	Phe	Leu		
			100					105					110				
ctg	ttg	gtg	atg	gcc	tat	gac	cgc	tat	gtg	gcc	atc	tgt	aag	ccc	ttg	384	
Leu	Leu	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu		
		115					120					125					
cat	tat	ttg	gtt	atc	atg	aga	caa	tgg	gtg	tgt	gtt	ttg	ctg	ctg	gta	432	
His	Tyr	Leu	Val	Ile	Met	Arg	Gln	Trp	Val	Cys	Val	Leu	Leu	Leu	Val		
		130				135					140						
gtg	tcc	tgg	gtt	gga	gga	ttt	ctg	caa	tca	gta	ttt	caa	ctt	agc	att	480	
Val	Ser	Trp	Val	Gly	Gly	Phe	Leu	Gln	Ser	Val	Phe	Gln	Leu	Ser	Ile		
145				150						155					160		
att	tat	ggg	ctc	cca	ttc	tgt	ggc	ccc	aat	gtc	att	gat	cat	ttt	ttc	528	
Ile	Tyr	Gly	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His	Phe	Phe		
				165				170						175			
tgt	gac	atg	tat	ccc	tta	ttg	aaa	ctg	gcc	tgc	act	gac	acc	cat	gtt	576	
Cys	Asp	Met	Tyr	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Thr	Asp	Thr	His	Val		
			180					185					190				
att	ggc	ctc	tta	gtg	gtg	gcc	aat	gga	gga	ctg	tct	tgc	act	att	gcg	624	
Ile	Gly	Leu	Leu	Val	Val	Ala	Asn	Gly	Gly	Leu	Ser	Cys	Thr	Ile	Ala		
		195					200					205					
ttt	ctg	ctc	tta	ctc	atc	tct	tat	ggg	gtc	atc	ctg	cac	tct	cta	aag	672	
Phe	Leu	Leu	Leu	Ile	Ser	Tyr	Gly	Val	Ile	Leu	His	Ser	Leu	Lys			
		210				215					220						
aaa	ctt	aga	tca	agc	agt	gaa	ggg	agg	cac	aaa	gcc	tta	tcc	acc	tgt	720	
Lys	Leu	Arg	Ser	Ser	Ser	Glu	Gly	Arg	His	Lys	Ala	Leu	Ser	Thr	Cys		
225					230					235					240		
ggc	tcc	cat	atc	act	gtg	gtg	atc	ctc	ttc	ttt	gtc	cct	tgt	att	ttc	768	
Gly	Ser	His	Ile	Thr	Val	Val	Ile	Leu	Phe	Phe	Val	Pro	Cys	Ile	Phe		
				245					250					255			
atg	tat	gtg	aga	cct	cct	ttg	acc	tta	ccc	att	gat	aaa	tcc	ttg	act	816	
Met	Tyr	Val	Arg	Pro	Pro	Leu	Thr	Leu	Pro	Ile	Asp	Lys	Ser	Leu	Thr		
			260					265					270				
gtg	ttt	tac	act	gtt	atc	aca	cct	atg	ttg	aac	cct	cta	atc	tat	act	864	
Val	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Thr		
		275					280					285					
tta	aga	aat	gca	gag	atg	aaa	aat	gct	atg	aag	aag	ctc	tgg	act	aga	912	
Leu	Arg	Asn	Ala	Glu	Met	Lys	Asn	Ala	Met	Lys	Lys	Leu	Trp	Thr	Arg		
		290				295					300						

200/261

aaa aga aaa  
Lys Arg Lys  
305

921

<210> 176  
<211> 307  
<212> PRT  
<213> Homo sapiens

<400> 176  
Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr  
1 5 10 15  
Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe  
20 25 30  
Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr  
35 40 45  
Val Ser Glu Thr Leu Gly Ser Pro Met Ser Phe Phe Leu Ala Gly Leu  
50 55 60  
Thr Phe Ile Asp Ile Ile Tyr Ser Ser Ser Ile Ser Pro Arg Leu Ile  
65 70 75 80  
Ser Asp Leu Phe Phe Gly Asn Asn Ser Ile Ser Phe Gln Ser Phe Met  
85 90 95  
Ala Gln Leu Phe Ile Glu His Leu Phe Gly Gly Ser Glu Val Phe Leu  
100 105 110  
Leu Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
115 120 125  
His Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val  
130 135 140  
Val Ser Trp Val Gly Gly Phe Leu Gln Ser Val Phe Gln Leu Ser Ile  
145 150 155 160  
Ile Tyr Gly Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe  
165 170 175  
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr His Val  
180 185 190  
Ile Gly Leu Leu Val Val Ala Asn Gly Gly Leu Ser Cys Thr Ile Ala  
195 200 205  
Phe Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys  
210 215 220  
Lys Leu Arg Ser Ser Ser Glu Gly Arg His Lys Ala Leu Ser Thr Cys  
225 230 235 240  
Gly Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe  
245 250 255  
Met Tyr Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr  
260 265 270  
Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr  
275 280 285  
Leu Arg Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg  
290 295 300  
Lys Arg Lys  
305

<210> 177  
<211> 939  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(939)

201/261

&lt;400&gt; 177

atg ttg cgg tcc acg gtg gtc aca cag caa ttc ctc ctt ctg gga ctc	48
Met Leu Arg Ser Thr Val Val Thr Gln Gln Phe Leu Leu Leu Gly Leu	
1 5 10 15	
tca gag gat cca gaa ctg cag acc atc ctt gct ggg ctg tcc ctg tcc	96
Ser Glu Asp Pro Glu Leu Gln Thr Ile Leu Ala Gly Leu Ser Leu Ser	
20 25 30	
atg tat ctg gtc acg gtg ctg agg aac ctg ctc agc atc ctg gct gtc	144
Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val	
35 40 45	
agc tct gac tcc cac ccc cac aca ccc atg tac ttc ttc ctc tcc aac	192
Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn	
50 55 60	
ctg tgc tgg gct gac atc ggt ttc acc ttg gcc acg gtt ccc aaa atg	240
Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met	
65 70 75 80	
att gtg gac atg ggg tcg cat agc aaa gtc atc tct tat ggg ggc tgc	288
Ile Val Asp Met Gly Ser His Ser Lys Val Ile Ser Tyr Gly Gly Cys	
85 90 95	
ctg aca cag atg tct ttc ttg gta ctt ttt gca tgt ata gta gac atg	336
Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met	
100 105 110	
ttc ctg act gtg atg gct tat gac tgc ttt gta gcc atc tgt cgc cct	384
Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro	
115 120 125	
ctg cac tac cca gtc atc gtg aat cct cac ctc tgt gtc ttc ttc gtt	432
Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val	
130 135 140	
ttg gtg tcc ttt ttc ctt agc ctg ttg gat tcc cag ctg cac agt tgg	480
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp	
145 150 155 160	
att gtg tta caa ttc acc ttc ttc aag aat gtg gaa atc tct aat ttt	528
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe	
165 170 175	
gtc tgt gag cca tct caa ctt ctc aag ctt gcc tct tat gac agc gtc	576
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val	
180 185 190	
atc aat agc ata ttc ata tat ttt gat aat act atg ttt ggt ttt ctt	624
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu	
195 200 205	
ccc att tca ggg atc ctt ttg tct tac tat aaa att gtc ccc tcc att	672
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile	
210 215 220	
cta agg att tca tca tca gat ggg aag tac aaa gcc ttc tca gcc tgt	720
Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys	
225 230 235 240	

202/261

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ggc tgt cac ctg gca gtt gtt tgc tta ttt tat gga aca ggc att ggc 768
Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
                245                250                255

gtg tac ctg act tca gct gtg gca cca ccc ctc agg aat ggt atg gtg 816
Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
                260                265                270

gcg tca gtg atg tac gct gtg gtc acc ccc atg ctg aac cct ttc atc 864
Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
                275                280                285

tac agc ctg aga aac agg gac att caa agt gcc ctg tgg agg gtg tgc 912
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys
                290                295                300

aac aaa aca gtc gaa tct cat gat ctg 939
Asn Lys Thr Val Glu Ser His Asp Leu
305                310

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<210> 178
<211> 313
<212> PRT
<213> Homo sapiens

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<400> 178
Met Leu Arg Ser Thr Val Val Thr Gln Gln Phe Leu Leu Leu Gly Leu
1      5      10      15
Ser Glu Asp Pro Glu Leu Gln Thr Ile Leu Ala Gly Leu Ser Leu Ser
20     25     30
Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
35     40     45
Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn
50     55     60
Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met
65     70     75     80
Ile Val Asp Met Gly Ser His Ser Lys Val Ile Ser Tyr Gly Gly Cys
85     90     95
Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met
100    105    110
Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
115    120    125
Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val
130    135    140
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
145    150    155    160
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
165    170    175
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val
180    185    190
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu
195    200    205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
210    215    220
Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys
225    230    235    240
Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
245    250    255
Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
260    265    270

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203/261

Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile  
           275                                  280                  285  
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys  
           290                                  295                  300  
 Asn Lys Thr Val Glu Ser His Asp Leu  
 305                                  310

<210> 179  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (945)

<400> 179  
 atg gaa gag gaa aat gca aca ttg ctg aca gag ttt gtt ctc aca gga 48  
 Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
   1                                  5                                  10                                  15  
  
 ctt tta tat caa cca cag tgg aaa ata ccc ctg ttc ctg aca ttc ttg 96  
 Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu  
                                   20                                  25                                  30  
  
 gta ata tat ctc atc acc atc atg ggg aat ctt ggt ctg att gct gtc 144  
 Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val  
                                   35                                  40                                  45  
  
 atc tgg aaa gac cct cac ctt cag atc cca atg tac tta ctc ctc ggg 192  
 Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly  
                                   50                                  55                                  60  
  
 aat tta gct ttt gta gat gct tgg ata tca tct aca gtg act cca aag 240  
 Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys  
                                   65                                  70                                  75                                  80  
  
 atg ctg aat aac ttc tta gct aag agt aag atg atg ata tct ctc tct 288  
 Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Met Ile Ser Leu Ser  
                                   85                                  90                                  95  
  
 gaa tgc atg gta caa ttt ttt tcc ttt gta atc agt gta acc aca gaa 336  
 Glu Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu  
                                   100                                  105                                  110  
  
 tgt ttt atc tcg gca tca atg gca tat gat cgc tat gta gcc att tgc 384  
 Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
                                   115                                  120                                  125  
  
 aaa gct tta ctt tat cca gtc att atg acc aac gga cta tgc atc cag 432  
 Lys Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln  
                                   130                                  135                                  140  
  
 cta tta gtc ttg tca ttt ata ggt ggc ctt ctt cat gct tta atc cat 480  
 Leu Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His  
                                   145                                  150                                  155                                  160  
  
 gaa att ttt tta ttc aga tta acc ttc tgt aat tcc aac ata ata caa 528  
 Glu Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln  
                                   165                                  170                                  175

204/261

cac ttt tac tgt gac att atc cca ttg tta aag att tcc tgt act gat 576  
 His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp  
 180 185 190

tct ttt att aac ttt cta atg gtt ttt att ttc gca gat tca att caa 624  
 Ser Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln  
 195 200 205

gtt ttt acc att gga act att ctt ata tct tat aca ctt gtc ctc ctt 672  
 Val Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu  
 210 215 220

ata atc tta aaa aat aag tct gtc aaa ggg ata caa aaa gct gtc tcc 720  
 Ile Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser  
 225 230 235 240

acc tgt gga gct cat ctc tta tct gta tct tta tac tat ggg ccc ctt 768  
 Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu  
 245 250 255

gtc ttc atg tat gtg ggc tct gca tcc ccg caa gca gat gac caa gat 816  
 Val Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp  
 260 265 270

atg atg gag tct cta ttt tac act gtc atc gtt cct tta tta aat tcc 864  
 Met Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser  
 275 280 285

atg atc tac agc ctg aga aac aag caa gta ata gct tca ttc aca aaa 912  
 Met Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys  
 290 295 300

atg ttc aaa aga aat gtt gct tcc aaa tct tgg 945  
 Met Phe Lys Arg Asn Val Ala Ser Lys Ser Trp  
 305 310 315

&lt;210&gt; 180

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val  
 35 40 45  
 Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly  
 50 55 60  
 Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Met Ile Ser Leu Ser  
 85 90 95  
 Glu Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu  
 100 105 110  
 Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Lys Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln  
 130 135 140

205/261

Leu Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His  
 145 150 155 160  
 Glu Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln  
 165 170 175  
 His Phe Tyr Cys Asp Ile Ile Pro Leu Lys Ile Ser Cys Thr Asp  
 180 185 190  
 Ser Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln  
 195 200 205  
 Val Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu  
 210 215 220  
 Ile Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu  
 245 250 255  
 Val Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp  
 260 265 270  
 Met Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser  
 275 280 285  
 Met Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys  
 290 295 300  
 Met Phe Lys Arg Asn Val Ala Ser Lys Ser Trp  
 305 310 315

<210> 181  
 <211> 927  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(927)

<400> 181  
 atg gtg aat aga aac aat gtg aca gag ttt att cta ctg ggg ctt ata 48  
 Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile  
 1 5 10 15  
 gag aat cca aaa atg cag aaa atc ata ttt gtt gtg ttt ttt gtc atc 96  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile  
 20 25 30  
 tac atc acc acc atg ata gga aat gtg ctc att gtg gtc acc gtc act 144  
 Tyr Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr  
 35 40 45  
 gcc agc cca tca ttg agg tcc ccc atg tac ttt tac ctg gcc tat ctg 192  
 Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu  
 50 55 60  
 tcc ttt att gat gcc tgc tat tcc tcc gtc aat gcc cct aag ctg atc 240  
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile  
 65 70 75 80  
 aca gat tca ctc tat gaa aac aag act atc tta ctc aat gga tgt atg 288  
 Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met  
 85 90 95  
 act caa gtc ttt gga gaa cat ttt ttc gga ggt gtt gag gtc atc cta 336  
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu  
 100 105 110

206/261

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ctt act gta atg gcc tat gac cgc tac gtg gtc atc tgc aag ccc ttg 384
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu
115 120 125

cac tat acc acc atc atg aag cag cat gtt tgt agc ctg cta gtg gga 432
His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
130 135 140

gtg tca tgg gta gga ggc ttt ctt cat gca acc gta cag atc ctc ttc 480
Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe
145 150 155 160

atc ttc caa tta cct ttc tgt ggt cct aat gtc ata gat cac ttt atg 528
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
165 170 175

tgg gat ctc aac cct ttg ctc aat ctt gtc tgc act aat acc cac act 576
Trp Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr
180 185 190

cta gga ctc ttc gtt gct gcc aac agt ggg ttc ata tgc ctg tta aac 624
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
195 200 205

ttt ctc ttg ctc ctg gtc tcc tat atg gtc ata ctg tac tcc tta agg 672
Phe Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg
210 215 220

acc cac agc tta gag gca agg tgc aaa gcc ctc tcc acc tgt gtc tcc 720
Thr His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser
225 230 235 240

cac atc aca gtt gtc atc tta ttc ttt ata ccc tgc ata ttt gtg tac 768
His Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr
245 250 255

atg aga cct cca gct act tta ccc att gat aaa gca gtt gct gta ttc 816
Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
260 265 270

tac act atg ata gct cct atg tta aac ccc tta atc tac acc ttg agg 864
Tyr Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275 280 285

aat gct cag atg aaa aat gcc att agg aaa ttg tgt agt agg aaa gct 912
Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala
290 295 300

att tca agt gtc aaa
Ile Ser Ser Val Lys
305

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&lt;210&gt; 182

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 182

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Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
1 5 10 15

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207/261

Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile  
                   20                  25                  30  
 Tyr Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr  
                   35                  40                  45  
 Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu  
                   50                  55                  60  
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile  
 65                  70                  75                  80  
 Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met  
                   85                  90                  95  
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu  
                   100                  105                  110  
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu  
                   115                  120                  125  
 His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly  
                   130                  135                  140  
 Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe  
 145                  150                  155                  160  
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
                   165                  170                  175  
 Trp Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr  
                   180                  185                  190  
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
                   195                  200                  205  
 Phe Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg  
                   210                  215                  220  
 Thr His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser  
 225                  230                  235                  240  
 His Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr  
                   245                  250                  255  
 Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe  
                   260                  265                  270  
 Tyr Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
                   275                  280                  285  
 Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala  
                   290                  295                  300  
 Ile Ser Ser Val Lys  
 305

<210> 183  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(948)

<400> 183  
 atg gga aga tgg gtg aac cag tcc tac aca gat ggc ttc ttc ctc ttg 48  
 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
   1                  5                  10                  15  
  
 ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96  
 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val  
                   20                  25                  30  
  
 atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144  
 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
                   35                  40                  45

208/261

ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc	192
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu	
50 55 60	
agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca	240
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro	
65 70 75 80	
aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg	288
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val	
85 90 95	
ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag	336
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu	
100 105 110	
ggg ctc ttg ctg gga ctc atg gct tat gac cgc tac gtg gcc gtt agc	384
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser	
115 120 125	
cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag	432
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln	
130 135 140	
att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag	480
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln	
145 150 155 160	
atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat	528
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp	
165 170 175	
cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac	576
His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp	
180 185 190	
act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt	624
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu	
195 200 205	
ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc tct cta	672
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Ser Leu	
210 215 220	
ggg gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg	720
Gly Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu	
225 230 235 240	
gcc acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca	768
Ala Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala	
245 250 255	
gcc atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat	816
Ala Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His	
260 265 270	
gac aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac	864
Asp Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn	
275 280 285	

ccc ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg 912  
Pro Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg  
290 295 300

aag ggg ctg gac cgc tgc agg att ggc agc cag cac 948  
Lys Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His  
305 310 315

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<210> 184
<211> 316
<212> PRT
<213> Homo sapiens
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<400>	184														
Met	Gly	Arg	Trp	Val	Asn	Gln	Ser	Tyr	Thr	Asp	Gly	Phe	Phe	Leu	Leu
1				5					10					15	
Gly	Ile	Phe	Ser	His	Ser	Gln	Thr	Asp	Leu	Val	Leu	Phe	Ser	Ala	Val
			20					25					30		
Met	Val	Val	Phe	Thr	Val	Ala	Leu	Cys	Gly	Asn	Val	Leu	Leu	Ile	Phe
		35					40				45				
Leu	Ile	Tyr	Leu	Asp	Ala	Gly	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Gln	Leu	Ser	Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Asn	Ile	Val	Pro
65					70					75					80
Lys	Met	Ala	Ala	Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val
				85					90					95	
Gly	Cys	Gly	Ile	Gln	Ile	Gly	Phe	Phe	Val	Ser	Leu	Val	Gly	Ser	Glu
			100					105					110		
Gly	Leu	Leu	Leu	Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Ser
			115				120					125			
His	Pro	Leu	His	Tyr	Pro	Ile	Leu	Met	Asn	Gln	Arg	Val	Cys	Leu	Gln
	130					135					140				
Ile	Thr	Gly	Ser	Ser	Trp	Ala	Phe	Gly	Ile	Ile	Asp	Gly	Val	Ile	Gln
145					150					155					160
Met	Val	Ala	Ala	Met	Gly	Leu	Pro	Tyr	Cys	Gly	Ser	Arg	Ser	Val	Asp
				165					170					175	
His	Phe	Phe	Cys	Glu	Val	Gln	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ala	Asp
			180						185				190		
Thr	Ser	Leu	Phe	Asp	Thr	Leu	Leu	Phe	Ala	Cys	Cys	Val	Phe	Met	Leu
		195					200					205			
Leu	Leu	Pro	Phe	Ser	Ile	Ile	Met	Ala	Ser	Tyr	Ala	Cys	Ile	Ser	Leu
	210					215					220				
Gly	Ala	Val	Leu	Arg	Ile	Arg	Ser	Ala	Gln	Ala	Trp	Lys	Lys	Ala	Leu
225					230					235					240
Ala	Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Ala
				245					250					255	
Ala	Met	Phe	Met	Tyr	Leu	Arg	Pro	Arg	Arg	Tyr	Arg	Ala	Pro	Ser	His
			260						265				270		
Asp	Lys	Val	Ala	Ser	Ile	Phe	Tyr	Thr	Val	Leu	Thr	Pro	Met	Leu	Asn
		275					280					285			
Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Gly	Glu	Val	Met	Gly	Ala	Leu	Arg
	290					295					300				
Lys	Gly	Leu	Asp	Arg	Cys	Arg	Ile	Gly	Ser	Gln	His				
305					310					315					

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<210> 185
<211> 942
<212> DNA
<213> Homo sapiens
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210/261

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (942)

&lt;400&gt; 185

gag act act aat acc act gga ttt gta aat gag ttc atc ctc ttg ggc	48
Glu Thr Thr Asn Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly	
1 5 10 15	
ttc ccc tgc cgc tgg gag atc cag atc ctc ctt ttt gtg gtc ttc tct	96
Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser	
20 25 30	
ctc atc tac ctt ctg acc ctc cta ggt aac aca tcc atc atc tgt gct	144
Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala	
35 40 45	
gtg tgg tca agc cag aaa ctc cac aca cct atg tac atc cta ctg gcc	192
Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala	
50 55 60	
aat ttc tcc ttc ctg gag atc tgc tgt gtc agt tct gac gtg ccc ata	240
Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile	
65 70 75 80	
atg gca gcc aat ctc atc tcc cag aca cag agc atc tcc tgt gct ggc	288
Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly	
85 90 95	
tgc ctg ctc cgg ttc tac ttc ttc tcc atg tgt gct gca gag tgc tta	336
Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu	
100 105 110	
ttt ctg tca gtg atg tct ttt gat agg ttt cct gcc att tgt aga cct	384
Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro	
115 120 125	
ttg cac tat ccc acc tta atg acc cat cac gtt tgt gct cat att ttt	432
Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe	
130 135 140	
gtg atc ttc tgc tgg gtg ggt ggc tgt ctc tgg tta ttg acc cct ttg	480
Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu	
145 150 155 160	
aca cta ata tct cag gtc ctc ttt tgt ggt cca aac act atc gac cat	528
Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His	
165 170 175	
ttt ttc tgt gat ctg gca cct ttg ctg gca ctg tct tgt gct cca ata	576
Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile	
180 185 190	
cct gga att act ctg act tgt ggt atc att agc gct ctc atc atc ttt	624
Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe	
195 200 205	
ctt acc ttc ttg tat atc ctt ggg act tat ttc tgt gtt cta agc aca	672
Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr	
210 215 220	



211/261

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gtg cta cag gtg cct tca ggc tta gga agg cat aag gct ttc tca act 720
Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
225                230                235                240

tgt ggc tgt cac ctt gct gta gtg tct ctc ttc tat ggt tct ctt atg 768
Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
                245                250                255

gtg atg tat gtt agc cca ggt tct ggg gac tat cat ggg ata aag aaa 816
Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys
                260                265                270

ttt gtg acc ttg ttc tat act ttg tca act cca ttc ttt aat cct ctg 864
Phe Val Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu
                275                280                285

atc tac agt ttc cgg aac aag gat atg aaa gag gca cta aag aaa ttt 912
Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe
290                295                300

ctg agg aat cgc cac act agc tcc agg tgg 942
Leu Arg Asn Arg His Thr Ser Ser Arg Trp
305                310

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<210> 186  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

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<400> 186
Glu Thr Thr Asn Thr Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly
1      5      10      15
Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser
20      25      30
Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala
35      40      45
Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala
50      55      60
Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile
65      70      75      80
Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly
85      90      95
Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu
100     105     110
Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro
115     120     125
Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe
130     135     140
Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu
145     150     155     160
Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His
165     170     175
Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile
180     185     190
Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe
195     200     205
Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr
210     215     220
Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
225     230     235                240

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212/261

<400> 187																	
gag	act	act	aat	atc	act	gga	ttt	gtg	aat	gag	ttc	atc	ctc	ttg	ggc	48	
Glu	Thr	Thr	Asn	Ile	Thr	Gly	Phe	Val	Asn	Glu	Phe	Ile	Leu	Leu	Gly		
1				5					10					15			
ttc	ccc	tgc	cgc	tgg	gag	atc	cag	atc	ctc	ctt	ttt	gtg	gtc	ttc	tct	96	
Phe	Pro	Cys	Arg	Trp	Glu	Ile	Gln	Ile	Leu	Leu	Phe	Val	Val	Phe	Ser		
			20					25					30				
ctc	atc	tac	ctt	ctg	acc	ctc	cta	ggc	aac	aca	tcc	atc	atc	tgt	gct	144	
Leu	Ile	Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Thr	Ser	Ile	Ile	Cys	Ala		
		35					40					45					
gtg	tgg	tca	agc	cag	aaa	ctc	cac	aca	cct	atg	tac	atc	cta	ctg	gcc	192	
Val	Trp	Ser	Ser	Gln	Lys	Leu	His	Thr	Pro	Met	Tyr	Ile	Leu	Leu	Ala		
	50					55					60						
aat	ttc	tcc	ttc	ctg	gag	atc	tgc	tgt	gtc	agt	tct	gac	gtg	ccc	ata	240	
Asn	Phe	Ser	Phe	Leu	Glu	Ile	Cys	Cys	Val	Ser	Ser	Asp	Val	Pro	Ile		
65					70					75					80		
atg	gca	gcc	aat	ctc	atc	tcc	cag	aca	cag	agc	atc	tcc	tgt	gct	ggc	288	
Met	Ala	Ala	Asn	Leu	Ile	Ser	Gln	Thr	Gln	Ser	Ile	Ser	Cys	Ala	Gly		
				85					90					95			
tgc	ctg	ctc	cgg	ttc	tac	ttc	ttc	tcc	atg	tgt	gct	gca	gag	tgc	tta	336	
Cys	Leu	Leu	Arg	Phe	Tyr	Phe	Phe	Ser	Met	Cys	Ala	Ala	Glu	Cys	Leu		
			100					105					110				
ttt	ctg	tca	gtg	atg	tct	ttt	gat	agg	ttt	cct	gcc	att	tgt	aga	cct	384	
Phe	Leu	Ser	Val	Met	Ser	Phe	Asp	Arg	Phe	Pro	Ala	Ile	Cys	Arg	Pro		
		115					120					125					
ttg	cac	tat	ccc	acc	tta	atg	acc	cat	cac	gtt	tgt	gct	cat	att	ttt	432	
Leu	His	Tyr	Pro	Thr	Leu	Met	Thr	His	His	Val	Cys	Ala	His	Ile	Phe		
	130					135					140						
gtg	atc	ttc	tgc	tgg	gtg	ggc	ggc	tgt	ctc	tgg	tta	ttg	acc	cct	ttg	480	
Val	Ile	Phe	Cys	Trp	Val	Gly	Gly	Cys	Leu	Trp	Leu	Leu	Thr	Pro	Leu		
145					150					155					160		

213/261

aca cta ata tct cag gtg ctc ttt tgt ggt cca aac act atc gac cat 528  
 Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His  
 165 170 175

ttt ttc tgt gat ctg gca cct ttg ctg gca ctg tct tgt gct cca ata 576  
 Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile  
 180 185 190

cct gga att act ctg act tgt ggt atc att agc gct ctc atc atc ttt 624  
 Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe  
 195 200 205

ctt acc ttc ttg tat atc ctt ggg act tat ttc tgt gtt cta agc aca 672  
 Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr  
 210 215 220

gtg cta cag gtg cct tca ggc tta gga agg cat aag gct ttc tca act 720  
 Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240

tgt ggc tgt cac ctt gct gta gtg tct ctc ttc tat ggt tct ctt atg 768  
 Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met  
 245 250 255

gtg atg tat gtt agc cca ggt tct ggg gac tat cat ggg ata aag aaa 816  
 Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys  
 260 265 270

ttt gcg acc ttg ttc tat act ttg tca act cca ttc ttt aat cct ctg 864  
 Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu  
 275 280 285

atc tac agt ttc cgg aac aag gat atg aaa gag gca cta aag aaa ttt 912  
 Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe  
 290 295 300

ctg agg aat cgc cac act agc tcc agg tgg 942  
 Leu Arg Asn Arg His Thr Ser Ser Arg Trp  
 305 310

&lt;210&gt; 188

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

Glu Thr Thr Asn Ile Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser  
 20 25 30  
 Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala  
 35 40 45  
 Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala  
 50 55 60  
 Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile  
 65 70 75 80  
 Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly  
 85 90 95  
 Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu  
 100 105 110

214/261

Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro  
 115 120 125  
 Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe  
 130 135 140  
 Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu  
 145 150 155 160  
 Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His  
 165 170 175  
 Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile  
 180 185 190  
 Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe  
 195 200 205  
 Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr  
 210 215 220  
 Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met  
 245 250 255  
 Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys  
 260 265 270  
 Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe  
 290 295 300  
 Leu Arg Asn Arg His Thr Ser Ser Arg Trp  
 305 310

&lt;210&gt; 189

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(951)

&lt;400&gt; 189

atg gag tca gaa aga acc act atg gat ggc tca ccc gtc ttc tat cta 48  
 Met Glu Ser Glu Arg Thr Thr Met Asp Gly Ser Pro Val Phe Tyr Leu  
 1 5 10 15

ttg ggc atc ccc tct ctg cca gag acc ttc ttc ctc cct gtg ttt ttt 96  
 Leu Gly Ile Pro Ser Leu Pro Glu Thr Phe Phe Leu Pro Val Phe Phe  
 20 25 30

att ttc ctc ctc ttc tac ctt ctc atc ctg atg ggt aat gcc ctg atc 144  
 Ile Phe Leu Leu Phe Tyr Leu Leu Ile Leu Met Gly Asn Ala Leu Ile  
 35 40 45

ctg gtg gcc gtg gtg gca gag ccc agc ctc cac aag ccc atg tac ttc 192  
 Leu Val Ala Val Val Ala Pro Ser Leu His Lys Pro Met Tyr Phe  
 50 55 60

ttt ctg atc aat ctc tcc acc ttg gac atc ctt ttc acc aca acc act 240  
 Phe Leu Ile Asn Leu Ser Thr Leu Asp Ile Leu Phe Thr Thr Thr Thr  
 65 70 75 80

gtc ccc aag atg ctg tcc tta ttc ttg ctt ggg gac cgc ttc ctc agc 288  
 Val Pro Lys Met Leu Ser Leu Phe Leu Leu Gly Asp Arg Phe Leu Ser  
 85 90 95

215/261

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ttt tct tcc tgc tta ctg cag atg tac ctc ttc caa agt ttt aca tgt 336
Phe Ser Ser Cys Leu Leu Gln Met Tyr Leu Phe Gln Ser Phe Thr Cys
100 105 110

tca gaa gcc ttc atc ctg gtg gtc atg gcc tat gac cgc tat gtg gct 384
Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala
115 120 125

atc tgc cac cca ctg cac tac cct gtc ctc atg aac cca cag acc aat 432
Ile Cys His Pro Leu His Tyr Pro Val Leu Met Asn Pro Gln Thr Asn
130 135 140

gct acc ttg gca gcc agt gcc tgg cta act gcc ctc ctc ctg ccc atc 480
Ala Thr Leu Ala Ala Ser Ala Trp Leu Thr Ala Leu Leu Leu Pro Ile
145 150 155 160

cca gca gta gta agg acc tcc cag atg gca tat aac agc att gcc tac 528
Pro Ala Val Val Arg Thr Ser Gln Met Ala Tyr Asn Ser Ile Ala Tyr
165 170 175

atc tac cac tgc ttc tgt gat cat ctg gct gtg gtc cag gcc tcc tgc 576
Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser Cys
180 185 190

tct gac acc acc ccc cag acc ctc atg ggc ttc tgc atc gcc atg gtg 624
Ser Asp Thr Thr Pro Gln Thr Leu Met Gly Phe Cys Ile Ala Met Val
195 200 205

gtg tcc ttc ctc ccc ctt ctc ctg gtg ctt ctc tcc tat gtc cac atc 672
Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Val His Ile
210 215 220

ctg gcc tca gtg ctt cgc atc agt tcc cta gaa gga cgg gca aaa gcc 720
Leu Ala Ser Val Leu Arg Ile Ser Ser Leu Glu Gly Arg Ala Lys Ala
225 230 235 240

ttc tcc acc tgc agc tcc cac ctt ctg gtc gtg ggc acc tac tac tca 768
Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Gly Thr Tyr Tyr Ser
245 250 255

tct att gcc ata gcc tac gtg gcc tac agg gct gac ctg ccc ctt gac 816
Ser Ile Ala Ile Ala Tyr Val Ala Tyr Arg Ala Asp Leu Pro Leu Asp
260 265 270

ttc cat atc atg ggc aat gtg gta tat gcc att ctc aca cca att ctc 864
Phe His Ile Met Gly Asn Val Val Tyr Ala Ile Leu Thr Pro Ile Leu
275 280 285

aac ccc ctc att tac acg ctg aga aac agg gat gta aag gca gcc atc 912
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Asp Val Lys Ala Ala Ile
290 295 300

acc aaa atc atg tct caa gac cca ggc tgt gac agg agc 951
Thr Lys Ile Met Ser Gln Asp Pro Gly Cys Asp Arg Ser
305 310 315

```

&lt;210&gt; 190

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

216/261

&lt;400&gt; 190

```

Met Glu Ser Glu Arg Thr Thr Met Asp Gly Ser Pro Val Phe Tyr Leu
 1          5          10          15
Leu Gly Ile Pro Ser Leu Pro Glu Thr Phe Phe Leu Pro Val Phe Phe
          20          25          30
Ile Phe Leu Leu Phe Tyr Leu Leu Ile Leu Met Gly Asn Ala Leu Ile
          35          40          45
Leu Val Ala Val Val Ala Glu Pro Ser Leu His Lys Pro Met Tyr Phe
          50          55          60
Phe Leu Ile Asn Leu Ser Thr Leu Asp Ile Leu Phe Thr Thr Thr Thr
65          70          75          80
Val Pro Lys Met Leu Ser Leu Phe Leu Leu Gly Asp Arg Phe Leu Ser
          85          90          95
Phe Ser Ser Cys Leu Leu Gln Met Tyr Leu Phe Gln Ser Phe Thr Cys
          100          105          110
Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala
          115          120          125
Ile Cys His Pro Leu His Tyr Pro Val Leu Met Asn Pro Gln Thr Asn
          130          135          140
Ala Thr Leu Ala Ala Ser Ala Trp Leu Thr Ala Leu Leu Leu Pro Ile
145          150          155          160
Pro Ala Val Val Arg Thr Ser Gln Met Ala Tyr Asn Ser Ile Ala Tyr
          165          170          175
Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser Cys
          180          185          190
Ser Asp Thr Thr Pro Gln Thr Leu Met Gly Phe Cys Ile Ala Met Val
          195          200          205
Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Val His Ile
          210          215          220
Leu Ala Ser Val Leu Arg Ile Ser Ser Leu Glu Gly Arg Ala Lys Ala
225          230          235          240
Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Gly Thr Tyr Tyr Ser
          245          250          255
Ser Ile Ala Ile Ala Tyr Val Ala Tyr Arg Ala Asp Leu Pro Leu Asp
          260          265          270
Phe His Ile Met Gly Asn Val Val Tyr Ala Ile Leu Thr Pro Ile Leu
          275          280          285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Asp Val Lys Ala Ala Ile
          290          295          300
Thr Lys Ile Met Ser Gln Asp Pro Gly Cys Asp Arg Ser
305          310          315

```

&lt;210&gt; 191

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(969)

&lt;400&gt; 191

```

atg cct tct atc aat gac acc cac ttc tat ccc ccc ttc ttc ctc ctg      48
Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1          5          10          15

cta gga ata cca gga ctg gac act tta cat atc tgg att tct ttc cca      96
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20          25          30

```

217/261

ttc tgt att gtg tac ctg att gcc att gtg ggg aat atg acc att ctc	144
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu	
35 40 45	
ttt gtg atc aaa act gaa cat agt cta cac cag ccc atg ttc tac ttc	192
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe	
50 55 60	
ctg gcc atg ttg tct atg att gat ctg ggt ctg tcc aca tcc act atc	240
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile	
65 70 75 80	
ccc aaa atg cta gga atc ttc tgg ttc aac ctc caa gag atc agc ttt	288
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe	
85 90 95	
ggg gga tgc ctt ctt cag atg ttc ttt att cac atg ttt aca ggc atg	336
Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met	
100 105 110	
gag act gtt ctg ttg gtg gtc atg gct tat gac cgc ttt gtt gcc atc	384
Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile	
115 120 125	
tgc aac cct ctc cag tac acc atg atc ctc acc aat aaa acc atc agt	432
Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser	
130 135 140	
atc cta gct tct gtg gtt gtt gga aga aat tta gtt ctt gta acc cca	480
Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro	
145 150 155 160	
ttt gtg ttt ctc att ctg cgt ctg cca ttc tgt ggg cat aac atc gta	528
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val	
165 170 175	
cct cac aca tac tgt gag cac agg ggt ctg gcc ggg ttg gcc tgt gca	576
Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala	
180 185 190	
ccc att aag atc aac ata atc tat ggg ctc atg gtg att tct tat att	624
Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile	
195 200 205	
att gtg gat gtg atc tta att gcc tct tcc tat gtg ctt atc ctt aga	672
Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg	
210 215 220	
gct gtt ttt cgc ctt ccc tct caa gat gtc cga cta aag gcc ttc aat	720
Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn	
225 230 235 240	
acc tgt ggt tct cat gtc tgt gtt atg ctg tgc ttt tac aca cca gca	768
Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala	
245 250 255	
ttt ttt tct ttt atg aca cat cgt ttt ggc caa aac att ccc cac tat	816
Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr	
260 265 270	

218/261

atc cat att ctt ttg gct aac ctg tat gtg gtt gtc cca cct gcc ctt 864  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu  
 275 280 285

aac cct gtc att tat gga aga tat gaa ata cat tgt atg aga aat aag 912  
 Asn Pro Val Ile Tyr Gly Arg Tyr Glu Ile His Cys Met Arg Asn Lys  
 290 295 300

gat tta aag gca gca aaa aag aag ctt atc cat cgg att tgg aaa atg 960  
 Asp Leu Lys Ala Ala Lys Lys Lys Leu Ile His Arg Ile Trp Lys Met  
 305 310 315 320

ggt aaa aac 969  
 Gly Lys Asn

<210> 192  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 192  
 Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu  
 1 5 10 15  
 Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro  
 20 25 30  
 Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu  
 35 40 45  
 Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe  
 50 55 60  
 Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile  
 65 70 75 80  
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe  
 85 90 95  
 Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met  
 100 105 110  
 Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser  
 130 135 140  
 Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro  
 145 150 155 160  
 Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val  
 165 170 175  
 Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala  
 180 185 190  
 Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile  
 195 200 205  
 Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg  
 210 215 220  
 Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala  
 245 250 255  
 Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Gly Arg Tyr Glu Ile His Cys Met Arg Asn Lys  
 290 295 300



219/261

Asp Leu Lys Ala Ala Lys Lys Lys Leu Ile His Arg Ile Trp Lys Met  
 305 310 315 320  
 Gly Lys Asn

<210> 193  
 <211> 954  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(954)

<400> 193  
 atg ctt ccc tct aat atc acc tca aca cat cca gct gtc ttt ttg ttg 48  
 Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu  
 1 5 10 15  
 gta gga att cct ggt ttg gaa cac ctg cat gcc tgg atc tcc atc ccc 96  
 Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro  
 20 25 30  
 ttc tgc ttt gct tat act ctg gcc ctg cta ggc aac tgt acc ctt ctc 144  
 Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu  
 35 40 45  
 ttc att atc cgg gct gat gca gcc ctc cat gaa ccc atg tac ctc ttt 192  
 Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe  
 50 55 60  
 ctg gcc atg ttg gca acc att gac ttg gtt ctt tct tct aca acg ctg 240  
 Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu  
 65 70 75 80  
 ccc aaa atg ctt gcc ata ttc tgg ttc agg gat cag gag atc aac ttc 288  
 Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe  
 85 90 95  
 ttt gcc tgt ctg gtc cag atg ttc ttc ctt cac tcc ttc tcc atc atg 336  
 Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met  
 100 105 110  
 gag tca gca gtg ctg ctg gcc atg gcc ttt gac cgc tat gtg gcc atc 384  
 Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 tgc aag cca ttg cac tac acg acg gtc ctg act ggg tcc ctc atc acc 432  
 Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr  
 130 135 140  
 aag att ggc atg gct gct gtg gcc tgg gct gtg aca cta atg act cca 480  
 Lys Ile Gly Met Ala Ala Val Ala Trp Ala Val Thr Leu Met Thr Pro  
 145 150 155 160  
 ctc ccc ttc ctg ctc aga cgc ttc cac tac tgc cga ggc cca gtg att 528  
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile  
 165 170 175

220/261

```

gcc cat tgc tac tgt gaa cac atg gct gtg gta agg ctg gcg tgt ggg 576
Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
180 185 190

gac act agc ttc aac aat atc tat ggc att gct gtg gcc atg ttt att 624
Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
195 200 205

gtg gtg ttg gac ctg ctc ttt gtt atc ctg tct tat gtc ttc atc ctt 672
Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
210 215 220

cag gca gtt ctc cag ctt gcc tct cag gag gcc cgc tac aag gca ttt 720
Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
225 230 235 240

ggg aca tgt gtg tct cac ata ggt gcc atc ctg tcc acc tac act cca 768
Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
245 250 255

gta gtc atc tct tca gtc atg cac cgt gta gcc cgc cat gct gcc cct 816
Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
260 265 270

cgt gtc cac ata ctc ctt gct att ttc tat ctc ctt ttc cca ccc atg 864
Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
275 280 285

gtc aat cct atc ata tat gga gtc aag acc aag cag att cgc aga agt 912
Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Arg Ser
290 295 300

ttg att aag gca gtt tca acg ttg cga gca aca tgt act aca 954
Leu Ile Lys Ala Val Ser Thr Leu Arg Ala Thr Cys Thr Thr
305 310 315

```

&lt;210&gt; 194

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

```

Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu
1 5 10 15
Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro
20 25 30
Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
35 40 45
Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
50 55 60
Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe
85 90 95
Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
100 105 110
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115 120 125
Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr
130 135 140

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221/261

Lys Ile Gly Met Ala Ala Val Ala Trp Ala Val Thr Leu Met Thr Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile  
 165 170 175  
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly  
 180 185 190  
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile  
 195 200 205  
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu  
 210 215 220  
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro  
 245 250 255  
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro  
 260 265 270  
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met  
 275 280 285  
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Arg Ser  
 290 295 300  
 Leu Ile Lys Ala Val Ser Thr Leu Arg Ala Thr Cys Thr Thr  
 305 310 315

<210> 195  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)... (948)

<400> 195  
 atg gca gta cga aac ggg act ttt ctt ctc ctt ttt gtc ctt cct ggc 48  
 Met Ala Val Arg Asn Gly Thr Phe Leu Leu Leu Phe Val Leu Pro Gly  
 1 5 10 15  
 atc cct ggg ttg gag gct tat cac att tgg ctg tca ata cct ctt tgc 96  
 Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro Leu Cys  
 20 25 30  
 ctc att tac atc act gca gtc ctg gga aac agc atc ctg ata gtg gtt 144  
 Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile Val Val  
 35 40 45  
 att gtc atg gaa cgt aac ctt cat gtg ccc atg tat ttc ttc ctc tca 192  
 Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 atg ctg gcc gtc atg gac atc ctg ctg tct acc acc act gtg ccc aag 240  
 Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys  
 65 70 75 80  
 gcc cta gcc atc ttt tgg ctt caa gca cat aac att gct ttt gat gcc 288  
 Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe Asp Ala  
 85 90 95  
 tgt gtc acc caa ggc ttc ttt gtc cat atg atg ttt gtg ggg gag tca 336  
 Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly Glu Ser  
 100 105 110

222/261

```

gct atc ctg tta gcc atg gcc ttt gat cgc ttt gtg gcc att tgt gcc 384
Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys Ala
      115                      120                      125

cca ctg aga tat aca aca gtg cta aca tgg cct gtt gtg ggg agg att 432
Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly Arg Ile
      130                      135                      140

gct ctg gcc gtc atc acc cga agc ttc tgc atc atc ttc cca gtc ata 480
Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro Val Ile
145                      150                      155                      160

ttc ttg ctg aag cgg ctg ccc ttc tgc cta acc aac att gtt cct cac 528
Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val Pro His
      165                      170                      175

tcc tac tgt gag cat att gga gtg gct cgt tta gcc tgt gct gac atc 576
Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala Asp Ile
      180                      185                      190

act gtt aac att tgg tat ggc ttc tca gtg ccc att gtc atg gtc atc 624
Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met Val Ile
      195                      200                      205

ttg gat gtt atc ctc atc gct gtg tct tac tca ctg atc ctc cga gca 672
Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu Arg Ala
      210                      215                      220

gtg ttt cgt ttg ccc tcc cag gat gct cgg cac aag gcc ctc agc act 720
Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu Ser Thr
225                      230                      235                      240

tgt ggc tcc cac ctc tgt gtc atc ctt atg ttt tat gtt cca tcc ttc 768
Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro Ser Phe
      245                      250                      255

ttt acc tta ttg acc cat cat ttt ggg cgt aat att cct caa cat gtc 816
Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln His Val
      260                      265                      270

cat atc ttg ctg gcc aat ctt tat gtg gca gtg cca cca atg ctg aac 864
His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met Leu Asn
      275                      280                      285

ccc att gtc tat ggt gtg aag act aag cag ata cgt gag gaa tta aag 912
Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Glu Leu Lys
      290                      295                      300

aga aaa ttt tct agc ttt att ttc ctg aaa ttc cgg 948
Arg Lys Phe Ser Ser Phe Ile Phe Leu Lys Phe Arg
305                      310                      315

```

&lt;210&gt; 196

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

```

Met Ala Val Arg Asn Gly Thr Phe Leu Leu Leu Phe Val Leu Pro Gly
 1              5              10              15

```

223/261

```

Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro Leu Cys
      20      25      30
Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile Val Val
      35      40      45
Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys
      65      70      75      80
Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe Asp Ala
      85      90      95
Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly Glu Ser
      100      105      110
Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys Ala
      115      120      125
Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly Arg Ile
      130      135      140
Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro Val Ile
      145      150      155      160
Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val Pro His
      165      170      175
Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala Asp Ile
      180      185      190
Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met Val Ile
      195      200      205
Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu Arg Ala
      210      215      220
Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro Ser Phe
      245      250      255
Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln His Val
      260      265      270
His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met Leu Asn
      275      280      285
Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Glu Leu Lys
      290      295      300
Arg Lys Phe Ser Ser Phe Ile Phe Leu Lys Phe Arg
      305      310      315

```

&lt;210&gt; 197

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(963)

&lt;400&gt; 197

```

atg tca gat tcc aac ctc agt gat aac cat ctt cca gac acc ttc ttc 48
Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
1      5      10      15

```

```

tta aca ggg atc cca ggg ctg gag gct gcc cac ttc tgg att gcc atc 96
Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile
      20      25      30

```

```

cct ttc tgt gcc atg tat ctt gta gca ctg gtt gga aat gct gcc ctc 144
Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
      35      40      45

```

224/261

atc	ctg	gtc	att	gcc	atg	gac	aat	gct	ctt	cat	gca	cct	atg	tac	ctc	192
Ile	Leu	Val	Ile	Ala	Met	Asp	Asn	Ala	Leu	His	Ala	Pro	Met	Tyr	Leu	
	50					55					60					
ttc	ctc	tgc	ctt	ctc	tca	ctc	aca	gac	ctg	gct	ctc	agt	tct	acc	act	240
Phe	Leu	Cys	Leu	Leu	Ser	Leu	Thr	Asp	Leu	Ala	Leu	Ser	Ser	Thr	Thr	
	65				70				75						80	
gtg	ccc	aag	atg	ctg	gcc	att	ttg	tgg	ctc	cat	gct	ggg	gag	att	tcc	288
Val	Pro	Lys	Met	Leu	Ala	Ile	Leu	Trp	Leu	His	Ala	Gly	Glu	Ile	Ser	
				85				90						95		
ttt	ggg	gga	tgc	ctg	gcc	cag	atg	ttt	tgt	gtc	cat	tct	atc	tat	gct	336
Phe	Gly	Gly	Cys	Leu	Ala	Gln	Met	Phe	Cys	Val	His	Ser	Ile	Tyr	Ala	
			100					105						110		
ctg	gag	tcc	tgc	att	cta	ctt	gcc	atg	gcc	ttt	gat	agg	tat	gtg	gct	384
Leu	Glu	Ser	Ser	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	
			115				120					125				
atc	tgt	aac	cca	tta	agg	tat	aca	acc	att	ctc	aac	cat	gct	gtc	ata	432
Ile	Cys	Asn	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Asn	His	Ala	Val	Ile	
	130					135					140					
ggc	aga	att	ggc	ttt	gtt	ggg	cta	ttc	cgt	agt	gtg	gct	att	gtc	tcc	480
Gly	Arg	Ile	Gly	Phe	Val	Gly	Leu	Phe	Arg	Ser	Val	Ala	Ile	Val	Ser	
	145				150				155						160	
ccc	ttc	atc	ttc	ttg	ctg	agg	cga	ctc	ccc	tac	tgt	ggg	cac	cgt	gtc	528
Pro	Phe	Ile	Phe	Leu	Leu	Arg	Arg	Leu	Pro	Tyr	Cys	Gly	His	Arg	Val	
				165				170						175		
atg	aca	cac	aca	tac	tgt	gag	cat	atg	ggc	atc	gcc	cga	ctg	gcc	tgt	576
Met	Thr	His	Thr	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg	Leu	Ala	Cys	
			180					185					190			
gcc	aac	atc	act	gtc	aat	att	gtc	tat	ggg	cta	act	gtg	gct	ctg	ctg	624
Ala	Asn	Ile	Thr	Val	Asn	Ile	Val	Tyr	Gly	Leu	Thr	Val	Ala	Leu	Leu	
	195						200					205				
gcc	atg	gga	ctg	gat	tcc	att	ctc	att	gcc	att	tcc	tat	ggc	ttt	atc	672
Ala	Met	Gly	Leu	Asp	Ser	Ile	Leu	Ile	Ala	Ile	Ser	Tyr	Gly	Phe	Ile	
	210					215					220					
ctc	cat	gca	gtc	ttt	cac	ctt	cca	tct	cat	gat	gcc	cag	cac	aaa	gct	720
Leu	His	Ala	Val	Phe	His	Leu	Pro	Ser	His	Asp	Ala	Gln	His	Lys	Ala	
	225				230					235					240	
ctg	agt	acc	tgt	ggc	tcc	cac	att	ggc	atc	atc	ctg	gtt	ttc	tac	atc	768
Leu	Ser	Thr	Cys	Gly	Ser	His	Ile	Gly	Ile	Ile	Leu	Val	Phe	Tyr	Ile	
				245				250						255		
cct	gcc	ttc	ttc	tcc	ttc	ctc	acc	cac	cgc	ttt	ggg	cac	cac	gaa	gtc	816
Pro	Ala	Phe	Phe	Ser	Phe	Leu	Thr	His	Arg	Phe	Gly	His	His	Glu	Val	
			260					265					270			
ccc	aag	cat	gtg	cac	atc	ttt	ctg	gct	aat	ctc	tat	gtg	ctg	gtg	cct	864
Pro	Lys	His	Val	His	Ile	Phe	Leu	Ala	Asn	Leu	Tyr	Val	Leu	Val	Pro	
		275					280					285				

225/261

cct gta ctc aat cct att ctc tat gga gct aga acc aag gag att cgg 912  
 Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg  
 290 295 300

aga agg acg tta gag agg ttg att ccc tgt cca ttt att ttc tct gat 960  
 Arg Arg Thr Leu Glu Arg Leu Ile Pro Cys Pro Phe Ile Phe Ser Asp  
 305 310 315 320

cac 963  
 His

<210> 198  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe  
 1 5 10 15  
 Leu Thr Gly Ile Pro Gly Leu Glu Ala His Phe Trp Ile Ala Ile  
 20 25 30  
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu  
 35 40 45  
 Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu  
 50 55 60  
 Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr  
 65 70 75 80  
 Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser  
 85 90 95  
 Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala  
 100 105 110  
 Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile  
 130 135 140  
 Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser  
 145 150 155 160  
 Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val  
 165 170 175  
 Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys  
 180 185 190  
 Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu  
 195 200 205  
 Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile  
 210 215 220  
 Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala  
 225 230 235 240  
 Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile  
 245 250 255  
 Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val  
 260 265 270  
 Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro  
 275 280 285  
 Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg  
 290 295 300  
 Arg Arg Thr Leu Glu Arg Leu Ile Pro Cys Pro Phe Ile Phe Ser Asp  
 305 310 315 320  
 His

226/261

<210> 199  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(948)

<400> 199  
 atg ccc aaa ggc aac tca tgt ttt aac cca acc tcc ttt ctg ctc atg 48  
 Met Pro Lys Gly Asn Ser Cys Phe Asn Pro Thr Ser Phe Leu Leu Met  
 1 5 10 15

gga att cca ggc ccg gag gca tcc cac ttt tgg att gct ttt ccc ttc 96  
 Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro Phe  
 20 25 30

tgc tcc atg tat gcc ctg gca gtg ctg gga aac atg gtg gtg ctg cta 144  
 Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu Leu  
 35 40 45

gtg gta cat tca gag cct gta ttg cac cag ccc atg tac ctg ttc ctc 192  
 Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe Leu  
 50 55 60

tgc atg cta tcc acc att gac ctg gtc ctc tgc acc tcc act gtg ccc 240  
 Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val Pro  
 65 70 75 80

aag ctc ctt gca ctt ttt tgg gca aag gat gct gag atc aac ttt ggg 288  
 Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe Gly  
 85 90 95

gcc tgt gct gcc cag atg ttc ttt atc cat ggc ttc tca gct gta gaa 336  
 Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val Glu  
 100 105 110

tct ggt ata ctg cta gca atg gcc ttt gac cgc tac tta gcc att tgc 384  
 Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile Cys  
 115 120 125

tgg cct ctg cac tat ggg tca ttg ctc tcc cca gag tct gta ggc aag 432  
 Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly Lys  
 130 135 140

ctg ggg gct gca gcc gtg ctt cgt ggt ttg gga ctc atg acc cca ctc 480  
 Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro Leu  
 145 150 155 160

acc tgc tta ctg gca aga ctg agc tac tgc agt cga gtg gtg gcc cac 528  
 Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala His  
 165 170 175

tcc tac tgt gaa cac atg gct gtg gta aag ctg gct tgt gga gga aca 576  
 Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly Thr  
 180 185 190

cag cca aac aac atc tat ggc atc act gct gcc aca ctg gtg gtg ggc 624  
 Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val Gly  
 195 200 205



227/261

act gac tcc atc tgt att gct gtc tcc tat gca ctc atc ctc cga gct 672  
 Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg Ala  
 210 215 220

gtg tta ggt ctt tcc tcc aag gag gca agg gct aag acc ttt ggc act 720  
 Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly Thr  
 225 230 235 240

tgt ggc tcc cac ctg ggt gtc ata ctt ctc ttc tac aca cca gga ctc 768  
 Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly Leu  
 245 250 255

ttc tcc ttc tac aca cag cgg ttt ggc cag cac gtg ccc cgg cac atc 816  
 Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His Ile  
 260 265 270

cac atc ctt cta gct gac ctc tac ctg gtt gtg cca ccc atg ctc aac 864  
 His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu Asn  
 275 280 285

ccc atc atc tat ggc atg aag acc aaa cag atc tgg gat ggg gcc ctc 912  
 Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala Leu  
 290 295 300

cgg ctt ctg aag aag aaa aaa ttc tcc tca aag ctg 948  
 Arg Leu Leu Lys Lys Lys Lys Phe Ser Ser Lys Leu  
 305 310 315

&lt;210&gt; 200

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 200

Met Pro Lys Gly Asn Ser Cys Phe Asn Pro Thr Ser Phe Leu Leu Met  
 1 5 10 15  
 Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro Phe  
 20 25 30  
 Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu Leu  
 35 40 45  
 Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe Leu  
 50 55 60  
 Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val Pro  
 65 70 75 80  
 Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe Gly  
 85 90 95  
 Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val Glu  
 100 105 110  
 Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile Cys  
 115 120 125  
 Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly Lys  
 130 135 140  
 Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro Leu  
 145 150 155 160  
 Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala His  
 165 170 175  
 Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly Thr  
 180 185 190  
 Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val Gly  
 195 200 205

228/261

Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg Ala  
 210 215 220  
 Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly Leu  
 245 250 255  
 Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His Ile  
 260 265 270  
 His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu Asn  
 275 280 285  
 Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala Leu  
 290 295 300  
 Arg Leu Leu Lys Lys Lys Lys Phe Ser Ser Lys Leu  
 305 310 315

&lt;210&gt; 201

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(948)

&lt;400&gt; 201

atg aat acc act cta ttt cat cct tac tct ttc ctt ctt ctg gga att 48  
 Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile  
 1 5 10 15

cct ggg ctg gaa agt atg cat ctc tgg gtt ggt ttt cct ttc ttt gct 96  
 Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala  
 20 25 30

gtg ttc ctg aca gct gtc ctt ggg aat atc acc atc ctt ttt gtg att 144  
 Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile  
 35 40 45

cag act gac agt agt ctc cat cat ccc atg ttc tac ttc ctg gcc att 192  
 Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile  
 50 55 60

ctg tca tct att gac ccg ggc ctg tct aca tcc acc atc cct aaa atg 240  
 Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met  
 65 70 75 80

ctt ggc acc ttc tgg ttt acc ctg aga gaa atc tcc ttt gaa gga tgc 288  
 Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys  
 85 90 95

ctt acc cag atg ttc ttc atc cac ctg tgc act ggc atg gaa tca gct 336  
 Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala  
 100 105 110

gtg ctt gtg gcc atg gcc tat gat tgc tat gtg gcc atc tgt gac cct 384  
 Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro  
 115 120 125

ctt tgc tac acg ttg gtg ctg aca aac aag gtg gtg tca gtt atg gca 432  
 Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala  
 130 135 140

229/261

ctg gcc atc ttt ctg aga ccc tta gtc ttt gtc ata ccc ttt gtt cta 480  
 Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu  
 145 150 155 160

ttt atc cta agg ctt cca ttt tgt gga cac caa att att cct cat act 528  
 Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr  
 165 170 175

tat ggt gag cac atg ggc att gcc cgc ctg tct tgt gcc agc atc agg 576  
 Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg  
 180 185 190

gtt aac atc atc tat ggc tta tgt gcc atc tct atc ctg gtc ttt gac 624  
 Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp  
 195 200 205

atc ata gca att gtc att tcc tat gta cag atc ctt tgt gct gta ttt 672  
 Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe  
 210 215 220

cta ctc tct tca cat gat gca cga ctc aag gca ttc agc acc tgt ggc 720  
 Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240

tct cat gtg tgt gtc atg ttg act ttc tat atg cct gca ttt ttc tca 768  
 Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser  
 245 250 255

ttc atg acc cat agg ttt gag aac tgg tca tct act caa ttt atg aaa 816  
 Phe Met Thr His Arg Phe Glu Asn Trp Ser Ser Thr Gln Phe Met Lys  
 260 265 270

atg atc acc ctg tcc aat ctc tat gtt gtg gtg cca cca atg ctc aat 864  
 Met Ile Thr Leu Ser Asn Leu Tyr Val Val Val Pro Pro Met Leu Asn  
 275 280 285

cct gtc ata tat gga gtc aga acc aag cag atc tat gtc tgc atg aat 912  
 Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Met Asn  
 290 295 300

aag gtg atc agg aag gaa tgc ata atc aag ctt tat 948  
 Lys Val Ile Arg Lys Glu Cys Ile Ile Lys Leu Tyr  
 305 310 315

&lt;210&gt; 202

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile  
 1 5 10 15  
 Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala  
 20 25 30  
 Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile  
 35 40 45  
 Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile  
 50 55 60  
 Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met  
 65 70 75 80

230/261

Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys  
                     85                    90                    95  
 Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala  
                     100                    105                    110  
 Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro  
                     115                    120                    125  
 Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala  
                     130                    135                    140  
 Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu  
                     145                    150                    155                    160  
 Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr  
                     165                    170                    175  
 Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg  
                     180                    185                    190  
 Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp  
                     195                    200                    205  
 Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe  
                     210                    215                    220  
 Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly  
                     225                    230                    235                    240  
 Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser  
                     245                    250                    255  
 Phe Met Thr His Arg Phe Glu Asn Trp Ser Ser Thr Gln Phe Met Lys  
                     260                    265                    270  
 Met Ile Thr Leu Ser Asn Leu Tyr Val Val Val Pro Pro Met Leu Asn  
                     275                    280                    285  
 Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Met Asn  
                     290                    295                    300  
 Lys Val Ile Arg Lys Glu Cys Ile Ile Lys Leu Tyr  
                     305                    310                    315

<210> 203  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(945)

<400> 203  
 atg aac aac tct gac act cgc ata gca ggc tgc ttc ctc act ggc atc 48  
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   1                    5                    10                    15  
  
 cct ggg ctg gag caa cta cat atc tgg ctg tcc atc ccc ttc tgc atc 96  
 Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile  
                     20                    25                    30  
  
 atg tac atc gct gcc ctg gaa ggc aat ggc atc cta att tgt gtc atc 144  
 Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile  
                     35                    40                    45  
  
 ctc tcc cag gca atc ctg cat gag ccc atg tac ata ttc tta tct atg 192  
 Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met  
                     50                    55                    60  
  
 ctg gcc agt gct gat gtc ttg ctc tct acc acc acc atg cct aag gcc 240  
 Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala  
                     65                    70                    75                    80

231/261

ctg gcc aat ttg tgg cta ggt tat agc cac att tcc ttt gat ggc tgc	288
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys	
85 90 95	
ctc act cag atg ttc ttc att cac ttc ctc ttc att cac tct gct gtc	336
Leu Thr Gln Met Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val	
100 105 110	
ctg ctg gcc atg gcc ttt gac cgc tat gtg gcc atc tgc tcc ccc ctg	384
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu	
115 120 125	
cga tat gtc aca atc ctc aca agc aag gtc att ggg aag atc gtc act	432
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr	
130 135 140	
gcc acc ctg agc cgc agc ttc atc att atg ttt cca tcc atc ttt ctc	480
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu	
145 150 155 160	
ctt gag cac ctg cac tat tgc cag atc aac atc att gca cac aca ttt	528
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe	
165 170 175	
tgt gag cac atg ggc att gcc cat ctg tcc tgt tct gat atc tcc atc	576
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile	
180 185 190	
aat gtc tgg tat ggg ttg gca gct gct ctt ctc tcc aca ggc ctg gac	624
Asn Val Trp Tyr Gly Leu Ala Ala Ala Leu Leu Ser Thr Gly Leu Asp	
195 200 205	
atc atg ctt att act gtt tcc tac atc cac atc ctc caa gca gtc ttc	672
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe	
210 215 220	
cgc ctc ctt tct caa gat gcc cgc tcc aag gcc ctg agt acc tgt gga	720
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly	
225 230 235 240	
tcc cat atc tgt gtc atc cta ctc ttc tat gtc cct gcc ctt ttt tct	768
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser	
245 250 255	
gtc ttt gcc tac agg ttt ggt ggg aga agc atc cca tgc tat gtc cat	816
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His	
260 265 270	
att ctc ctg gcc agc ctc tac gtt gtc att cct cct atg ctc aat ccc	864
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro	
275 280 285	
gtt att tat gga ctg aga gga aag gac caa aaa aat gca tta att agg	912
Val Ile Tyr Gly Leu Arg Gly Lys Asp Gln Lys Asn Ala Leu Ile Arg	
290 295 300	
tcc atg ttt gat gat cag aag cat ctg aaa aca	945
Ser Met Phe Asp Asp Gln Lys His Leu Lys Thr	
305 310 315	

&lt;210&gt; 204

232/261

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

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Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile
 1           5           10           15
Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
           20           25           30
Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
 35           40           45
Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
 50           55           60
Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
 65           70           75           80
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys
           85           90           95
Leu Thr Gln Met Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val
           100           105           110
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
           115           120           125
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr
 130           135           140
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu
 145           150           155           160
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe
           165           170           175
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile
           180           185           190
Asn Val Trp Tyr Gly Leu Ala Ala Leu Leu Ser Thr Gly Leu Asp
           195           200           205
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe
 210           215           220
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly
 225           230           235           240
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser
           245           250           255
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His
           260           265           270
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro
           275           280           285
Val Ile Tyr Gly Leu Arg Gly Lys Asp Gln Lys Asn Ala Leu Ile Arg
 290           295           300
Ser Met Phe Asp Asp Gln Lys His Leu Lys Thr
 305           310           315

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&lt;210&gt; 205

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(948)

&lt;400&gt; 205

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atg gct ctg gaa gct caa acc tct gtc tct gag ttt atc ctg atg gga 48
Met Ala Leu Glu Ala Gln Thr Ser Val Ser Glu Phe Ile Leu Met Gly
 1           5           10           15

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233/261

ttc cct ggc att cac act ttc ttg ttt ttt gtt ttt ttt ttg ttg ttg	96
Phe Pro Gly Ile His Thr Phe Leu Phe Phe Val Phe Phe Leu Leu Leu	
20 25 30	
ttg ttg ttt gtt tcc aca att gtg ggc aat ata act att ctg gtt gtt	144
Leu Leu Phe Val Ser Thr Ile Val Gly Asn Ile Thr Ile Leu Val Val	
35 40 45	
gtt gcc act gaa cca gtc ttg cac aag cct gtg tac ctt ttt ctg tgc	192
Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe Leu Cys	
50 55 60	
atg ctc tca acc atc gac ttg gct gcc tct gtc tcc aca gtt ccc aag	240
Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val Pro Lys	
65 70 75 80	
cta ctg gct atc ttc tgg tgt gga gcc gga cat ata tct gcc tct gcc	288
Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala Ser Ala	
85 90 95	
tgc ctg gca cag atg ttc ttc att cat gcc ttc tgc atg atg gag tcc	336
Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met Glu Ser	
100 105 110	
act gtg cta ctg gcc atg gcc ttt gat cgc tac gtg gcc atc tgc cac	384
Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His	
115 120 125	
cca ctc cgc tat gcc aca atc ctc act gac acc atc att gcc cac ata	432
Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala His Ile	
130 135 140	
ggg gtg gca gct gta gtg cga ggc tcc ctg ctc atg ctc cca tgt ccc	480
Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro Cys Pro	
145 150 155 160	
ttc ctt att ggg cgt ttg aac ttc tgc caa agc cat gtg atc cta cac	528
Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile Leu His	
165 170 175	
acg tac tgt gag cac atg gct gtg gtg aag ctg gcc tgt gga gac acc	576
Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Asp Thr	
180 185 190	
agg cct aac cgt gtg tat ggg ctg aca gct gca ctg ttg gtc att ggg	624
Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val Ile Gly	
195 200 205	
gtt gac ttg ttt tgc att ggt ctc tcc tat gcc cta agt gca caa gct	672
Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala Gln Ala	
210 215 220	
gtc ctt cgc ctc tca tcc cat gaa gct cgg tcc aag gcc cta ggg acc	720
Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu Gly Thr	
225 230 235 240	
tgt ggt tcc cat gtc tgt gtc atc ctc atc tct tat aca cca gcc ctc	768
Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu	
245 250 255	

234/261

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ttc tcc ttt ttt aca cac cgc ttt ggc cat cac gtt cca gtc cat att 816
Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val His Ile
      260                      265                      270

cac att ctt ttg gcc aat gtt tat ctg ctt ttg cca cct gct ctt aat 864
His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala Leu Asn
      275                      280                      285

cct gtg gta tat gga gtt aag acc aaa cag atc caa gga gta tgg aag 912
Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Gly Val Trp Lys
      290                      295                      300

gaa cta tcc tgg aaa gca cta cat tta act cct tcc 948
Glu Leu Ser Trp Lys Ala Leu His Leu Thr Pro Ser
305                      310                      315

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<210> 206
<211> 316
<212> PRT
<213> Homo sapiens

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<400> 206
Met Ala Leu Glu Ala Gln Thr Ser Val Ser Glu Phe Ile Leu Met Gly
 1      5      10      15
Phe Pro Gly Ile His Thr Phe Leu Phe Phe Val Phe Phe Leu Leu Leu
      20      25      30
Leu Leu Phe Val Ser Thr Ile Val Gly Asn Ile Thr Ile Leu Val Val
      35      40      45
Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe Leu Cys
      50      55      60
Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val Pro Lys
      65      70      75      80
Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala Ser Ala
      85      90      95
Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met Glu Ser
      100      105      110
Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His
      115      120      125
Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala His Ile
      130      135      140
Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro Cys Pro
      145      150      155      160
Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile Leu His
      165      170      175
Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Asp Thr
      180      185      190
Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val Ile Gly
      195      200      205
Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala Gln Ala
      210      215      220
Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu Gly Thr
      225      230      235      240
Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu
      245      250      255
Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val His Ile
      260      265      270
His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala Leu Asn
      275      280      285
Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Gly Val Trp Lys
      290      295      300

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235/261

Glu Leu Ser Trp Lys Ala Leu His Leu Thr Pro Ser  
 305 310 315

&lt;210&gt; 207

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(939)

&lt;400&gt; 207

atg gac aaa gaa aac tgg cta tcc cag cct tct ttt ctc ctg gta ggg 48  
 Met Asp Lys Glu Asn Trp Leu Ser Gln Pro Ser Phe Leu Leu Val Gly  
 1 5 10 15

att cca ggt tta gag gaa agc cag cac tgg att gca ctg ccc ctg ggc 96  
 Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu Pro Leu Gly  
 20 25 30

atc ctt tac ctc ctt gct tta gtg ggc aat gtt acc att ctc ttc atc 144  
 Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile Leu Phe Ile  
 35 40 45

atc tgg atg gac cca tcc ttg cac caa tct atg tac ctc ttc ctg tcc 192  
 Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu Phe Leu Ser  
 50 55 60

atg cta gct gcc atc gac ctg gtt ctg gcc tcc tcc act gca ccc aaa 240  
 Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr Ala Pro Lys  
 65 70 75 80

gcc ctt gca gtg ctc ctg gtt cat gcc cac gag att ggg tac atc gtc 288  
 Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly Tyr Ile Val  
 85 90 95

tgc ctg atc cag atg ttc ttc atc cat gca ttc tcc tcc atg gag tca 336  
 Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser Met Glu Ser  
 100 105 110

ggg gta ctt gtg gcc atg gct ctg gat cgc tat gta gcc att tgt cac 384  
 Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125

ccc ttg cac cat tcc aca atc ctg cat cca ggg gtc ata ggg cgc atc 432  
 Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile Gly Arg Ile  
 130 135 140

gga atg gtg gtg ctg gtg agg gga tta cta ctc ctt atc ccc ttc ccc 480  
 Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile Pro Phe Pro  
 145 150 155 160

att ttg ttg gga aca ctt atc ttc tgc caa gcc acc atc ata ggc cat 528  
 Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile Ile Gly His  
 165 170 175

gcc tat tgt gaa cat atg gct gtt gtg aaa ctt gcc tgc tca gaa acc 576  
 Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Ser Glu Thr  
 180 185 190

236/261

aca gtc aat cga gct tat ggg ctg act atg gcc ttg ctt gtg att ggg 624  
 Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu Val Ile Gly  
 195 200 205

ctg gat gtt ctg gcc att ggt gtt tcc tat gcc cac atc ctc cag gca 672  
 Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile Leu Gln Ala  
 210 215 220

gtg ctg aag gta cca ggg agt gag gcc cga ctt aag gcg ttt agc aca 720  
 Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala Phe Ser Thr  
 225 230 235 240

tgt ggc tct cat att tgt gtc atc ctg gtc ttc tat ctt aca gtc cag 768  
 Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Leu Thr Val Gln  
 245 250 255

ttc ata tat att tct cag aag aga att cct cca gat gtc ccc atc ctg 816  
 Phe Ile Tyr Ile Ser Gln Lys Arg Ile Pro Pro Asp Val Pro Ile Leu  
 260 265 270

ctc aac atc ctg cac cac ctt att ccc cca gct ctg aac ccc att gtt 864  
 Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val  
 275 280 285

tat ggt gtg aga acc aag gag atc aag cag gga atc cag aac ctg ctg 912  
 Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu  
 290 295 300

agg agg tta cac ata agt aag cat tgg 939  
 Arg Arg Leu His Ile Ser Lys His Trp  
 305 310

&lt;210&gt; 208

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 208

Met Asp Lys Glu Asn Trp Leu Ser Gln Pro Ser Phe Leu Leu Val Gly  
 1 5 10 15  
 Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu Pro Leu Gly  
 20 25 30  
 Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile Leu Phe Ile  
 35 40 45  
 Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr Ala Pro Lys  
 65 70 75 80  
 Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly Tyr Ile Val  
 85 90 95  
 Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser Met Glu Ser  
 100 105 110  
 Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile Gly Arg Ile  
 130 135 140  
 Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile Pro Phe Pro  
 145 150 155 160  
 Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile Ile Gly His  
 165 170 175

237/261

Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Ser Glu Thr  
 180 185 190  
 Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu Val Ile Gly  
 195 200 205  
 Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile Leu Gln Ala  
 210 215 220  
 Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Leu Thr Val Gln  
 245 250 255  
 Phe Ile Tyr Ile Ser Gln Lys Arg Ile Pro Pro Asp Val Pro Ile Leu  
 260 265 270  
 Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val  
 275 280 285  
 Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu  
 290 295 300  
 Arg Arg Leu His Ile Ser Lys His Trp  
 305 310

&lt;210&gt; 209

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(954)

&lt;400&gt; 209

atg aat aga aaa cag act gag gtc tct gag ttc atc ctg ctg gga ttc 48  
 Met Asn Arg Lys Gln Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 ccg ggc att cac agc tgg caa cac tgg cta tct ctg ccc ctg gca cta 96  
 Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu Ala Leu  
 20 25 30  
 ctg tat ctc tca gca ctt gct gca aac acc ctc atc ctc atc atc atc 144  
 Leu Tyr Leu Ser Ala Leu Ala Asn Thr Leu Ile Leu Ile Ile Ile  
 35 40 45  
 tgg cag aac cct tct tta cag cag ccc atg tat att ttc ctt ggc atc 192  
 Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu Gly Ile  
 50 55 60  
 ctc tgt atg gta gac atg ggt ctg gcc act act atc atc cct aag atc 240  
 Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro Lys Ile  
 65 70 75 80  
 ctg gcc atc ttc tgg ttt gat gcc aag gtt att agc ctc cct gag tgc 288  
 Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro Glu Cys  
 85 90 95  
 ttt gct cag att tat gcc att cac ttc ttt gtg ggc atg gag tct ggt 336  
 Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu Ser Gly  
 100 105 110  
 atc cta ctc tgc atg gct ttt gat aga tat gtg gct att tgt cac cct 384  
 Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 115 120 125

238/261

ctt cgc tat cca tca att gtc acc agt cat gct tgc gca ttg tta gct 432  
 Leu Arg Tyr Pro Ser Ile Val Thr Ser His Ala Cys Ala Leu Leu Ala  
 130 135 140

gtt ggg act gcc acc ttc ctg aga ggg gta tta ctc att att ccc ttt 480  
 Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro Phe  
 145 150 155 160

act ttc ctc acc aag cgc ctg ccc tac tgc aga ggc aat ata ctt ccc 528  
 Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu Pro  
 165 170 175

cat acc tac tgt gac cac atg tct gta gcc aaa ttg tcc tgt ggt aat 576  
 His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly Asn  
 180 185 190

gtc aag gtc aat gcc atc tat ggt ctg atg gtt gcc ctc ctg att ggg 624  
 Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly  
 195 200 205

ggc ttt gac ata ctg tgt atc acc atc tcc tat acc atg att ctc cgg 672  
 Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg  
 210 215 220

gca gtg gtc agc ctc tcc tca gca gat gct cgg cag aag gcc ttt aat 720  
 Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn  
 225 230 235 240

acc tgc act gcc cac att tgt gcc att gtt ttc tcc tat act cca gct 768  
 Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala  
 245 250 255

ttc ttc tcc ttc ttt tcc cac cgc ttt ggg gaa cac ata atc ccc cct 816  
 Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro Pro  
 260 265 270

tct tgc cac atc att gta gcc aat att tat ctg ctc cta cca ccc act 864  
 Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr  
 275 280 285

atg aac cct att gtc tat ggg gtg aaa acc aaa cag ata cga gac tgt 912  
 Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys  
 290 295 300

gtc ata agg atc ctt tca ggt tct aag gat acc aaa tcc tac 954  
 Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr  
 305 310 315

&lt;210&gt; 210

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 210

Met Asn Arg Lys Gln Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu Ala Leu  
 20 25 30  
 Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile Ile Ile  
 35 40 45

239/261

Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu Gly Ile  
 50 55 60  
 Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro Lys Ile  
 65 70 75 80  
 Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro Glu Cys  
 85 90 95  
 Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu Ser Gly  
 100 105 110  
 Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 115 120 125  
 Leu Arg Tyr Pro Ser Ile Val Thr Ser His Ala Cys Ala Leu Leu Ala  
 130 135 140  
 Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro Phe  
 145 150 155 160  
 Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu Pro  
 165 170 175  
 His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly Asn  
 180 185 190  
 Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly  
 195 200 205  
 Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg  
 210 215 220  
 Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala  
 245 250 255  
 Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro Pro  
 260 265 270  
 Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr  
 275 280 285  
 Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys  
 290 295 300  
 Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr  
 305 310 315

<210> 211  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(960)

<400> 211  
 atg gca ctt agc aat tcc agc tgg agg cta ccc cag cct tct ttt ttc 48  
 Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe  
 1 5 10 15  
 ctg gta gga att ccg ggt tta gag gaa agc cag cac tgg atc gca ctg 96  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 ccc ctg ggc atc ctt tac ctc ctt gct cta gtg ggc aat gtt acc att 144  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 ctc ttc atc atc tgg atg gac cca tcc ttg cac caa tct atg tac ctc 192  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60

240/261

ttc ctg tcc atg cta gct gcc atc gac ctg gtt gtg gcc tcc tcc act	240
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr	
65 70 75 80	
gca ccc aaa gcc ctt gca gtg ctc ctg gtt cgt gcc caa gag att ggt	288
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly	
85 90 95	
tac act gtc tgc ctg atc cag atg ttc ttc acc cat gca ttc tcc tcc	336
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser	
100 105 110	
atg gag tca ggg gta ctt gtg gcc atg gct ctg gat cgc tat gta gcc	384
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala	
115 120 125	
att tgt cac ccc ttg cac cat tcc aca atc ctg cat cca ggg gtc ata	432
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile	
130 135 140	
ggg cac atc gga atg gtg gtg ctg gtg cgg gga tta cta ctc ctc atc	480
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile	
145 150 155 160	
ccc ttc ctc att ctg ttg cga aaa ctt atc ttc tgc caa gcc acc atc	528
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile	
165 170 175	
ata ggc cat gcc tat tgt gaa cat atg gct gtt gtg aaa ctt gcc tgc	576
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys	
180 185 190	
tca gaa acc aca gtc aat cga gct tat ggg ctg act gtg gcc ttg ctt	624
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu	
195 200 205	
gtg gtt ggg ctg gat gtc ctg gcc att ggt gtt tcc tat gcc cac att	672
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile	
210 215 220	
ctc cag gca gtg ctg aag gta cca gga aat gag gcc cga ctt aag gcc	720
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala	
225 230 235 240	
ttt agc aca tgt ggc tct cat gtt tgt gtc atc ctg gtc ttc tat atc	768
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile	
245 250 255	
ccg gga atg ttc tcc ttc ctc act cac cgc ttt ggt cat cat gta ccc	816
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro	
260 265 270	
cat cac gtc cat gtt ctt ctg gcc ata ctg tat cgc ctt gtg cca cct	864
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro	
275 280 285	
gca ctc aat cct ctt gtc tat agg agg gtg aga aat aag gat att cat	912
Ala Leu Asn Pro Leu Val Tyr Arg Arg Val Arg Asn Lys Asp Ile His	
290 295 300	

241/261

gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt gca ccg ccc tta 960  
 Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu Ala Pro Pro Leu  
 305 310 315 320

<210> 212  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe  
 1 5 10 15  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr  
 65 70 75 80  
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly  
 85 90 95  
 Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser  
 100 105 110  
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile  
 130 135 140  
 Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile  
 145 150 155 160  
 Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile  
 165 170 175  
 Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys  
 180 185 190  
 Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu  
 195 200 205  
 Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile  
 210 215 220  
 Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile  
 245 250 255  
 Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro  
 260 265 270  
 His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro  
 275 280 285  
 Ala Leu Asn Pro Leu Val Tyr Arg Arg Val Arg Asn Lys Asp Ile His  
 290 295 300  
 Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu Ala Pro Pro Leu  
 305 310 315 320

<210> 213  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (951)

242/261

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<400> 213
atg gat agg aag aat caa tat cta ccc agc tcc ttc tgg ctc act ggc 48
Met Asp Arg Lys Asn Gln Tyr Leu Pro Ser Ser Phe Trp Leu Thr Gly
1 5 10 15

atc cca ggg ctg gag tcc cta cac gtc tgg ctc tcc atc ccc ttt ggc 96
Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro Phe Gly
20 25 30

tcc atg tac ctg gtg gct gtg gtg ggg aat gtg acc atc ctg gct gtg 144
Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu Ala Val
35 40 45

gta aag ata gaa cgc agc ctg cac cag ccc atg tac ttt ttc ttg tgc 192
Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe Leu Cys
50 55 60

atg ttg gct gcc att gac ctg gtt ctg tct act tcc act ata ccc aaa 240
Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile Pro Lys
65 70 75 80

ctt ctg gga atc ttc tgg ttc gga gac agc tca atc agc ttt agt gct 288
Leu Leu Gly Ile Phe Trp Phe Gly Asp Ser Ser Ile Ser Phe Ser Ala
85 90 95

tgt ttc act cag atg ttt ttt gtc cac tta gcc aca gct gtg gag acg 336
Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr Ala Val Glu Thr
100 105 110

ggg ctg ctg ctg acc atg gct ttt gac cgc tat gta gcc atc tgc aag 384
Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
115 120 125

cct cta cac tac aag aga att ctc acg cct caa gtg atg ctg gga atg 432
Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val Met Leu Gly Met
130 135 140

agt atg gcc atc acc atc aga gct atc ata gcc ata act cca ctg agt 480
Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile Thr Pro Leu Ser
145 150 155 160

tgg atg gtg agt cat cta cct ttc tgt ggc tcc aat gtg gtt gtc cac 528
Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn Val Val Val His
165 170 175

tcc tac tgt gag cac ata gct ttg gcc agg tta gca tgt gct gac ccc 576
Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala Cys Ala Asp Pro
180 185 190

gtg ccc agc agt ctc tac agt ctg att ggt tcc tct ctt atg gtg ggc 624
Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser Leu Met Val Gly
195 200 205

tct gat gtg gcc ttc att gct gcc tcc tat atc tta att ctc aag gca 672
Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu Ile Leu Lys Ala
210 215 220

gta ttt ggt ctc tcc tca aag act gct cag ttg aaa gca tta agc aca 720
Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys Ala Leu Ser Thr
225 230 235 240

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243/261

tgt ggc tcc cat gtg ggg gtt atg gct ttg tac tat cta cct ggg atg	768
Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr Leu Pro Gly Met	
245 250 255	
gca tcc atc tat gcg gcc tgg ttg ggg cag gat gta gtg ccc ttg cac	816
Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val Val Pro Leu His	
260 265 270	
acc caa gtc ctg cta gct gac ctg tac gtg atc atc cca gcc acc tta	864
Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile Pro Ala Thr Leu	
275 280 285	
aat ccc atc atc tat ggc atg agg acc aaa caa ctg cgg gag aga ata	912
Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu Arg Glu Arg Ile	
290 295 300	
tgg act tgc ctt acc agg ttt gcg ttt cat tct cat tgg	951
Trp Thr Cys Leu Thr Arg Phe Ala Phe His Ser His Trp	
305 310 315	

&lt;210&gt; 214

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 214

Met Asp Arg Lys Asn Gln Tyr Leu Pro Ser Ser Phe Trp Leu Thr Gly	
1 5 10 15	
Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro Phe Gly	
20 25 30	
Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu Ala Val	
35 40 45	
Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe Leu Cys	
50 55 60	
Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile Pro Lys	
65 70 75 80	
Leu Leu Gly Ile Phe Trp Phe Gly Asp Ser Ser Ile Ser Phe Ser Ala	
85 90 95	
Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr Ala Val Glu Thr	
100 105 110	
Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys	
115 120 125	
Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val Met Leu Gly Met	
130 135 140	
Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile Thr Pro Leu Ser	
145 150 155 160	
Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn Val Val Val His	
165 170 175	
Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala Cys Ala Asp Pro	
180 185 190	
Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser Leu Met Val Gly	
195 200 205	
Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu Ile Leu Lys Ala	
210 215 220	
Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys Ala Leu Ser Thr	
225 230 235 240	
Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr Leu Pro Gly Met	
245 250 255	
Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val Val Pro Leu His	
260 265 270	

244/261

Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile Pro Ala Thr Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu Arg Glu Arg Ile  
 290 295 300  
 Trp Thr Cys Leu Thr Arg Phe Ala Phe His Ser His Trp  
 305 310 315

<210> 215  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)... (948)

<400> 215  
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 Met Ala Leu Glu Asn Cys Glu His Tyr Pro Ile Phe Tyr Leu Thr Ser  
 1 5 10 15  
 ttt cct gga ttg gaa ggc atc aaa cac tgg att ttc atc ccc ttt ttc 96  
 Phe Pro Gly Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe  
 20 25 30  
 ttt atg tac atg gtt gcc atc tca ggc aat tgt ttc att ctg atc att 144  
 Phe Met Tyr Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile  
 35 40 45  
 att aag acc aac cct cgt ctg cac aca ccc atg tac tat cta cta tcc 192  
 Ile Lys Thr Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser  
 50 55 60  
 ttg ctg gcc ctc act gac ctg ggg ctg tgt gtg tcc acg ttg ccc acc 240  
 Leu Leu Ala Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr  
 65 70 75 80  
 act atg ggg atc ttc tgg ttt aac tcc cag agt atc tac ttt gga gcg 288  
 Thr Met Gly Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala  
 85 90 95  
 tgt caa atc cag atg ttc tgc atc cac tct ttt tcc ttc atg gag tcc 336  
 Cys Gln Ile Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser  
 100 105 110  
 tca gtg ctc ctc atg atg tcc ttt gac cgc ttt gtg gcc atc tgc cac 384  
 Ser Val Leu Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 cct ctg agg tat tcg gtc att atc act ggc cag caa gtg gtc aga gca 432  
 Pro Leu Arg Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala  
 130 135 140  
 ggc cta att gtc atc ttc cgg gga cct gtg gcc act atc cct att gtc 480  
 Gly Leu Ile Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val  
 145 150 155 160  
 ctc ctc ctg aag gct ttt ccc tac tgt gga tct gtg gtc ctc tcc cac 528  
 Leu Leu Leu Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His  
 165 170 175

245/261

tca ttt tgc ctg cac cag gaa gtg ata cag ctg gcc tgc aca gat acc 576  
 Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr  
 180 185 190

acc ttc aat aat ctg tat gga ctg atg gtg gta gtt ttc act gtg atg 624  
 Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met  
 195 200 205

ctg gac ctg gtg ctc atc gca ctg tcc tat gga ctc atc ctg cac aca 672  
 Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr  
 210 215 220

gta gca ggc ctg gcc tcc caa gag gag cag cgc cgt gcc ttt cag aca 720  
 Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr  
 225 230 235 240

tgc acc gct cat ctc tgt gct gtg cta gta ttc ttt gtg ccc atg atg 768  
 Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met  
 245 250 255

ggg ctg tcc ctg gtg cac cgt ttt ggg aag cat gcc cca cct gct att 816  
 Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile  
 260 265 270

cat ctt ctt atg gcc aat gtc tac ctt ttt gtg cct ccc atg ctt aac 864  
 His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn  
 275 280 285

cca atc ata tac agc att aag acc aag gag atc cac cgt gcc att atc 912  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile  
 290 295 300

aaa ctc cta ggc aga aag caa ata cca aag gaa tct 948  
 Lys Leu Leu Gly Arg Lys Gln Ile Pro Lys Glu Ser  
 305 310 315

<210> 216  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Met Ala Leu Glu Asn Cys Glu His Tyr Pro Ile Phe Tyr Leu Thr Ser  
 1 5 10 15  
 Phe Pro Gly Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe  
 20 25 30  
 Phe Met Tyr Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile  
 35 40 45  
 Ile Lys Thr Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser  
 50 55 60  
 Leu Leu Ala Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr  
 65 70 75 80  
 Thr Met Gly Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala  
 85 90 95  
 Cys Gln Ile Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser  
 100 105 110  
 Ser Val Leu Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala  
 130 135 140

246/261

Gly Leu Ile Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val  
 145 150 155 160  
 Leu Leu Leu Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His  
 165 170 175  
 Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met  
 195 200 205  
 Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr  
 210 215 220  
 Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr  
 225 230 235 240  
 Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met  
 245 250 255  
 Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile  
 260 265 270  
 His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn  
 275 280 285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile  
 290 295 300  
 Lys Leu Leu Gly Arg Lys Gln Ile Pro Lys Glu Ser  
 305 310 315

<210> 217  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(948)

<400> 217  
 atg gat agg aag tac agc agc gtt tct gct acc ttc ctg ctg agt ggc 48  
 Met Asp Arg Lys Tyr Ser Ser Val Ser Ala Thr Phe Leu Leu Ser Gly  
 1 5 10 15  
 atc cct ggg ctg gag cgc atg cac atc tgg atc tcc atc cca ctg tgc 96  
 Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile Ser Ile Pro Leu Cys  
 20 25 30  
 ttc atg tat ctg gtt tcc atc ccg ggc aac tgc aca att ctt ttt atc 144  
 Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys Thr Ile Leu Phe Ile  
 35 40 45  
 att aaa aca gag cgc tca ctt cat gaa cct atg tat ctc ttc ctg tcc 192  
 Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 atg ctg gct ctg att gac ctg ggt ctc tcc ctt tgc act ctc cct aca 240  
 Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu Cys Thr Leu Pro Thr  
 65 70 75 80  
 gtc ctg ggc atc ttt tgg gtt gga gca cga gaa att agc cat gat gcc 288  
 Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu Ile Ser His Asp Ala  
 85 90 95  
 tgc ttt gct cag ctc ttt ttc att cac tgc ttc tcc ttc ctc gag tcc 336  
 Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe Ser Phe Leu Glu Ser  
 100 105 110

247/261

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tct gtg cta ctg tct atg gcc ttt gac cgc ttt gtg gct atc tgc cac 384
Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe Val Ala Ile Cys His
      115                120                125

ccc ttg cac tat gtt tcc att ctc acc aac aca gtc att ggc agg att 432
Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr Val Ile Gly Arg Ile
      130                135                140

ggc ctg gtc tct ctg ggt cgt agt gta gca ctc att ttt cca tta cct 480
Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu Ile Phe Pro Leu Pro
      145                150                155                160

ttt atg ctc aaa aga ttc ccc tat tgt ggc tcc cca gtt ctc tca cat 528
Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser Pro Val Leu Ser His
      165                170                175

tct tat tgt ctc cac caa gaa gtg atg aaa ttg gcc tgt gcc gac atg 576
Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu Ala Cys Ala Asp Met
      180                185                190

aag gcc aac agc atc tac ggc atg ttt gtc atc gtc tct aca gtg ggt 624
Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile Val Ser Thr Val Gly
      195                200                205

ata gac tca ctg ctc atc ctc ttc tct tat gct ctg atc ctg cgc acc 672
Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala Leu Ile Leu Arg Thr
      210                215                220

gtg ctg tcc atc gcc tcc agg gct gag aga ttc aag gcc ctt aac acc 720
Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe Lys Ala Leu Asn Thr
      225                230                235                240

tgt gtt tcc cac atc tgt gct gtg ctg ctc ttc tac act ccc atg att 768
Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Thr Pro Met Ile
      245                250                255

ggc ctc tct gtc atc cat cgc ttt gga aag cag gca ccc cac ctg gtc 816
Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln Ala Pro His Leu Val
      260                265                270

cag gtg gtc atg ggt ttc atg tat ctt ctc ttt cct cct gtg atg aat 864
Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe Pro Pro Val Met Asn
      275                280                285

ccc att gtc tac agt gtg aag acc aaa cag atc cgg gat cga cta tgg 912
Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile Arg Asp Arg Leu Trp
      290                295                300

agg ctt agc tgt tct cat tct ggt cac cgg ggt tgg 948
Arg Leu Ser Cys Ser His Ser Gly His Arg Gly Trp
      305                310                315

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&lt;210&gt; 218

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 218

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Met Asp Arg Lys Tyr Ser Ser Val Ser Ala Thr Phe Leu Leu Ser Gly
  1              5              10              15

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248/261

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Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile Ser Ile Pro Leu Cys
      20      25      30
Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys Thr Ile Leu Phe Ile
      35      40      45
Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu Cys Thr Leu Pro Thr
      65      70      75      80
Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu Ile Ser His Asp Ala
      85      90      95
Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe Ser Phe Leu Glu Ser
      100      105      110
Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr Val Ile Gly Arg Ile
      130      135      140
Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu Ile Phe Pro Leu Pro
      145      150      155      160
Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser Pro Val Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu Ala Cys Ala Asp Met
      180      185      190
Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile Val Ser Thr Val Gly
      195      200      205
Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala Leu Ile Leu Arg Thr
      210      215      220
Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe Lys Ala Leu Asn Thr
      225      230      235      240
Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Thr Pro Met Ile
      245      250      255
Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln Ala Pro His Leu Val
      260      265      270
Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe Pro Pro Val Met Asn
      275      280      285
Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile Arg Asp Arg Leu Trp
      290      295      300
Arg Leu Ser Cys Ser His Ser Gly His Arg Gly Trp
      305      310      315

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<210> 219  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(963)

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<400> 219
atg aca acc cac aac tcc act ggt agc agc cac tca ctc ttc att ctg   48
Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
  1      5      10      15

ctg agc att cct ggc tta gaa gac cag cac aca tgg atg tct ctc ccc   96
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
      20      25      30

ttc ttt att tcc tac ctt gtt gct ttc ctt ggg aac agc ctc atc atc   144
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
      35      40      45

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249/261

ttc atc atc atc act gaa tgc agc ctc cac gaa ccc atg tac ctt ttc	192
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe	
50 55 60	
ctc tgc atg ctg gct gtg gct gac ctt atc ctg tct act acc act gtg	240
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val	
65 70 75 80	
ccc aag gcc cta gcc ata ttt tgg ttc tat gct gga gca ata tcc ctt	288
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu	
85 90 95	
ggc ggc tgt gtt acc caa atc ttc ttt atc cat gct acc ttc atc gag	336
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu	
100 105 110	
gaa tca gga att ctg ttg gcg atg gca ctt gac cgc tat gtg gcc atc	384
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile	
115 120 125	
tgt gat cca ctg cac tat acc aca gtg ctc agt cgt gca aaa atc aca	432
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr	
130 135 140	
aag att ggc ttg gct gtg gtc ctg aga agc ttc tgt gtg atc atg cca	480
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro	
145 150 155 160	
gat gtg ttt ctg gta aag cgg ctg cct ttc tgc cat agc aat ctg ctg	528
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu	
165 170 175	
cca cat acc tac tgt gag cac atg gct gtt gcc aag ttt gct tgt gct	576
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala	
180 185 190	
gat att cat gtc aat gtt tgg tat ggc ttg tct gtc ctt ctc tat act	624
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr	
195 200 205	
gta gtg cta gat gcc ttg ctt atc tta gtg tcc tat agc ttc atc ctg	672
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Tyr Ser Phe Ile Leu	
210 215 220	
tat aca ggc ttc cac ctc ccc tcc ccc caa gga gct cgg caa aag gct	720
Tyr Thr Gly Phe His Leu Pro Ser Pro Gln Gly Ala Arg Gln Lys Ala	
225 230 235 240	
ctg ggc aca tgt ggc tcc ccc ctc aga gtc att tcc atg ttc tac ttg	768
Leu Gly Thr Cys Gly Ser Pro Leu Arg Val Ile Ser Met Phe Tyr Leu	
245 250 255	
cct ggt att ttt acc ata att acc cag cgg ttt ggg cac cat gtt cct	816
Pro Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro	
260 265 270	
ctc cat aca cac att ttg ctg gct aat gtc tgc gtg ttg gct cct ccc	864
Leu His Thr His Ile Leu Leu Ala Asn Val Cys Val Leu Ala Pro Pro	
275 280 285	

250/261

atg ctg aac ccc atc att tat ggg atc aac acc agg cag att caa gag 912  
 Met Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu  
 290 295 300

tta caa tca cta cag aga aca gtt tgg agg ttc ttc aaa ata ctg aag 960  
 Leu Gln Ser Leu Gln Arg Thr Val Trp Arg Phe Phe Lys Ile Leu Lys  
 305 310 315 320

ata 963  
 Ile

<210> 220  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 220  
 Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu  
 1 5 10 15  
 Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro  
 20 25 30  
 Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile  
 35 40 45  
 Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe  
 50 55 60  
 Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val  
 65 70 75 80  
 Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu  
 85 90 95  
 Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu  
 100 105 110  
 Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr  
 130 135 140  
 Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro  
 145 150 155 160  
 Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu  
 165 170 175  
 Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala  
 180 185 190  
 Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr  
 195 200 205  
 Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Tyr Ser Phe Ile Leu  
 210 215 220  
 Tyr Thr Gly Phe His Leu Pro Ser Pro Gln Gly Ala Arg Gln Lys Ala  
 225 230 235 240  
 Leu Gly Thr Cys Gly Ser Pro Leu Arg Val Ile Ser Met Phe Tyr Leu  
 245 250 255  
 Pro Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro  
 260 265 270  
 Leu His Thr His Ile Leu Leu Ala Asn Val Cys Val Leu Ala Pro Pro  
 275 280 285  
 Met Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu  
 290 295 300  
 Leu Gln Ser Leu Gln Arg Thr Val Trp Arg Phe Phe Lys Ile Leu Lys  
 305 310 315 320  
 Ile



251/261

<210> 221  
 <211> 954  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(954)

<400> 221  
 atg gga gac tgg aat aac agt gat gct gtg gag ccc ata ttt atc ctg 48  
 Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu  
 1 5 10 15

agg ggt ttt cct gga ctg gag tat gtt cat tct tgg ctc tcc atc ctc 96  
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu  
 20 25 30

ttc tgt ctt gca tat ttg gta gca ttt atg ggt aat gtt acc atc ctg 144  
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu  
 35 40 45

tct gtc att tgg ata gaa tcc tct ctc cat cag ccc atg tat tac ttt 192  
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60

att tcc atc tta gca gtg aat gac ctg ggg atg tcc ctg tct aca ctt 240  
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu  
 65 70 75 80

ccc acc atg ctt gct gtg tta tgg ttg gat gct cca gag atc cag gca 288  
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala  
 85 90 95

agt gct tgc tat gct cag ctg ttc ttc atc cac aca ttc aca ttc ctg 336  
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu  
 100 105 110

gag tcc tca gtg ttg ctg gcc atg gcc ttt gac cgt ttt gtt gct atc 384  
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125

tgc cat cca ctg cac tac ccc acc atc ctc acc aac agt gta att ggc 432  
 Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly  
 130 135 140

aaa att ggt ttg gcc tgt ttg cta cga agc ttg gga gtt gta ctt ccc 480  
 Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro  
 145 150 155 160

aca cct ttg cta ctg aga cac tat cac tac tgc cat ggc aat gcc ctc 528  
 Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu  
 165 170 175

tct cac gcc ttc tgt ttg cac cag gat gtt cta aga tta tcc tgt aca 576  
 Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr  
 180 185 190

gat gcc agg acc aac agt att tat ggg ctt tgt gta gtc att gcc aca 624  
 Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr  
 195 200 205

252/261

cta ggt gtg gat tca atc ttc ata ctt ctt tct tat gtt ctg att ctt	672
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu	
210 215 220	
aat act gtg ctg gat att gca tct cgt gaa gag cag cta aag gca ctc	720
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu	
225 230 235 240	
aac aca tgt gta tcc cat atc tgt gtg gtg ctt atc ttc ttt gtg cca	768
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro	
245 250 255	
gtt att ggg gtg tca atg gtc cat cgc ttt ggg aag cat ctg tct ccc	816
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro	
260 265 270	
ata gtc cac atc ctc atg gca gac atc tac ctt ctt ctt ccc cca gtc	864
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val	
275 280 285	
ctt aac cct att gtc tat agt gtc aga aca aag cag att cct gca gct	912
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Pro Ala Ala	
290 295 300	
gtg agg aaa cat agg aga gcc aca cag atg agc aag aat cta	954
Val Arg Lys His Arg Arg Ala Thr Gln Met Ser Lys Asn Leu	
305 310 315	

&lt;210&gt; 222

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu	
1 5 10 15	
Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu	
20 25 30	
Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu	
35 40 45	
Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe	
50 55 60	
Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu	
65 70 75 80	
Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala	
85 90 95	
Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu	
100 105 110	
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile	
115 120 125	
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly	
130 135 140	
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro	
145 150 155 160	
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu	
165 170 175	
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr	
180 185 190	
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr	
195 200 205	

253/261

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Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
 210                215                220
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
225                230                235                240
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
                245                250                255
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
                260                265                270
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
                275                280                285
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Pro Ala Ala
                290                295                300
Val Arg Lys His Arg Arg Ala Thr Gln Met Ser Lys Asn Leu
305                310                315

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<210> 223  
 <211> 954  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(954)

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<400> 223
atg cct act gta aac cac agt ggc act agc cac aca gtc ttc cac ttg   48
Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
 1                5                10                15

ctg ggc atc cct ggc cta cag gac cag cac atg tgg att tct atc cca   96
Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
                20                25                30

ttc ttc att tcc tat gtc acc gcc ctt ctt ggg aac agc ctg ctc atc   144
Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
                35                40                45

ttc att atc ctc aca aag cgc agc ctc cat gaa ccc atg tac ctc ttc   192
Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
                50                55                60

ctc tgc atg ctg gct gga gca gac att gtc ctc tcc acg tgc acc att   240
Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
                65                70                75                80

cct cag gcc tta gct atc ttc tgg ttc cgt gct ggg gac atc tcc ctg   288
Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
                85                90                95

gat cgt tgc atc act cag ctc ttc ttc atc cat tcc acc ttc atc tct   336
Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
                100                105                110

gag tca ggg atc ttg ctg gtg atg gcc ttt gac cac tat att gcc ata   384
Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
                115                120                125

tgc tac cca ctg agg tac acc acc att ctt aca aat gct ctg atc aag   432
Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
                130                135                140

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254/261

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aaa att tgt gtg act gtc tct ctg aga agt tat ggt aca att ttc cct 480
Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
145                      150                      155                      160

atc ata ttt ctt tta aaa aga ttg act ttc tgc cag aat aat att att 528
Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
165                      170                      175

cca cac acc ttt tgt gaa cac att ggc cta gcc aaa tat gca tgt aat 576
Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
180                      185                      190

gac att cga ata aac att tgg tat ggg ttt tcc att cta atg tcg acg 624
Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
195                      200                      205

gtg gtc tta gat gtt gta cta att ttt att tcc tat atg ctg att ctc 672
Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
210                      215                      220

cat gct gtc ttc cac atg cct tct cca gat gct tgc cac aaa gct ctc 720
His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
225                      230                      235                      240

aac aca ttt ggc tcc cat gtc tgc atc atc atc ctc ttt tat ggg tct 768
Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
245                      250                      255

ggc atc ttc aca atc ctt acc cag agg ttt gga cgc cac att cca cct 816
Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
260                      265                      270

tgt atc cac atc ccg ttg gct aat gtc tgc att ctg gct cca cct atg 864
Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
275                      280                      285

ctg aat ccc att att tat ggg atc aaa acc aag caa atc cag gaa cag 912
Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
290                      295                      300

ttg cgt agg gca atg aaa caa gcc att gga aga ctg ata gtc 954
Leu Arg Arg Ala Met Lys Gln Ala Ile Gly Arg Leu Ile Val
305                      310                      315

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&lt;210&gt; 224

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 224

```

Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
1          5          10          15
Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
20          25          30
Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
35          40          45
Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
50          55          60
Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
65          70          75          80

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Pro	Gln	Ala	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Ala	Gly	Asp	Ile	Ser	Leu
				85					90					95	
Asp	Arg	Cys	Ile	Thr	Gln	Leu	Phe	Phe	Ile	His	Ser	Thr	Phe	Ile	Ser
			100					105					110		
Glu	Ser	Gly	Ile	Leu	Leu	Val	Met	Ala	Phe	Asp	His	Tyr	Ile	Ala	Ile
			115				120					125			
Cys	Tyr	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Asn	Ala	Leu	Ile	Lys
			130			135					140				
Lys	Ile	Cys	Val	Thr	Val	Ser	Leu	Arg	Ser	Tyr	Gly	Thr	Ile	Phe	Pro
145					150					155					160
Ile	Ile	Phe	Leu	Leu	Lys	Arg	Leu	Thr	Phe	Cys	Gln	Asn	Asn	Ile	Ile
				165					170					175	
Pro	His	Thr	Phe	Cys	Glu	His	Ile	Gly	Leu	Ala	Lys	Tyr	Ala	Cys	Asn
			180					185					190		
Asp	Ile	Arg	Ile	Asn	Ile	Trp	Tyr	Gly	Phe	Ser	Ile	Leu	Met	Ser	Thr
			195				200					205			
Val	Val	Leu	Asp	Val	Val	Leu	Ile	Phe	Ile	Ser	Tyr	Met	Leu	Ile	Leu
			210			215					220				
His	Ala	Val	Phe	His	Met	Pro	Ser	Pro	Asp	Ala	Cys	His	Lys	Ala	Leu
225					230					235					240
Asn	Thr	Phe	Gly	Ser	His	Val	Cys	Ile	Ile	Ile	Leu	Phe	Tyr	Gly	Ser
			245						250					255	
Gly	Ile	Phe	Thr	Ile	Leu	Thr	Gln	Arg	Phe	Gly	Arg	His	Ile	Pro	Pro
			260					265					270		
Cys	Ile	His	Ile	Pro	Leu	Ala	Asn	Val	Cys	Ile	Leu	Ala	Pro	Pro	Met
			275				280					285			
Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Ile	Lys	Thr	Lys	Gln	Ile	Gln	Glu	Gln
			290			295					300				
Leu	Arg	Arg	Ala	Met	Lys	Gln	Ala	Ile	Gly	Arg	Leu	Ile	Val		
305					310					315					

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<210> 225
<211> 930
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (930)
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BNSDOCID: <WO\_\_\_\_\_03000735A2 | >

256/261

ttc aat gct cca gga att tcc cct gat gcc tgt att gct caa gag ttt	288
Phe Asn Ala Pro Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe	
85 90 95	
ttc atc cat gga ttc tca gct atg gag tca tct gta ctt ctt ata atg	336
Phe Ile His Gly Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met	
100 105 110	
tcc ttt gat cgc ttt att gcc atc tgc aac ccc ctg aga tac act tcc	384
Ser Phe Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser	
115 120 125	
atc ctc acc agt gcc aga aaa tgt att ttc tgt att ttg gcc ttt tgg	432
Ile Leu Thr Ser Ala Arg Lys Cys Ile Phe Cys Ile Leu Ala Phe Trp	
130 135 140	
tac ttt gga ttc ctc gtt atc tac att cag tct ctc tat acc aga aac	480
Tyr Phe Gly Phe Leu Val Ile Tyr Ile Gln Ser Leu Tyr Thr Arg Asn	
145 150 155 160	
ttg aga tat tgc aag aaa aac caa tta tcc cat tcc tac tgt ctc cac	528
Leu Arg Tyr Cys Lys Lys Asn Gln Leu Ser His Ser Tyr Cys Leu His	
165 170 175	
cag gat gtc atg aag ttg gcc tgt tct gac aac aga att gat gtt atc	576
Gln Asp Val Met Lys Leu Ala Cys Ser Asp Asn Arg Ile Asp Val Ile	
180 185 190	
tat ggc ttt ttt gga gca ctc tgc ctt atg gta gac ttt att ctc att	624
Tyr Gly Phe Phe Gly Ala Leu Cys Leu Met Val Asp Phe Ile Leu Ile	
195 200 205	
gct gtg tct tac acc ctg atc ctc aag act gta ctg gga att gca tcc	672
Ala Val Ser Tyr Thr Leu Ile Leu Lys Thr Val Leu Gly Ile Ala Ser	
210 215 220	
aaa aag gag cag ctt aag gct ctc aat act tgt gtt tca cac atc tgt	720
Lys Lys Glu Gln Leu Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys	
225 230 235 240	
gca gtg atc atc ttc tac ctg ccc atc atc aac ctg gcc gtt gtc cac	768
Ala Val Ile Ile Phe Tyr Leu Pro Ile Ile Asn Leu Ala Val Val His	
245 250 255	
cgc ttt gcc cgg cat gtc tct ccc ctc att aat gtt ctc atg gca aat	816
Arg Phe Ala Arg His Val Ser Pro Leu Ile Asn Val Leu Met Ala Asn	
260 265 270	
gtt ctc cta ctt gta cct cca ctg acg aac cca att gtt tat tgt gta	864
Val Leu Leu Leu Val Pro Pro Leu Thr Asn Pro Ile Val Tyr Cys Val	
275 280 285	
aaa act aaa cag att aga gat gga cta aat gtt aaa tta aca aga aaa	912
Lys Thr Lys Gln Ile Arg Asp Gly Leu Asn Val Lys Leu Thr Arg Lys	
290 295 300	
ata aga tgt cgt gga gat	930
Ile Arg Cys Arg Gly Asp	
305 310	

&lt;210&gt; 226

257/261

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 226

```

Met Glu Ile Ser Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His
 1           5           10           15
Ala Asn Ile Trp Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala
 20           25           30
Ile Leu Gly Asn Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser
 35           40           45
Leu His Glu Pro Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp
 50           55           60
Leu Gly Leu Ser Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu
 65           70           75           80
Phe Asn Ala Pro Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe
 85           90           95
Phe Ile His Gly Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met
100           105           110
Ser Phe Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser
115           120           125
Ile Leu Thr Ser Ala Arg Lys Cys Ile Phe Cys Ile Leu Ala Phe Trp
130           135           140
Tyr Phe Gly Phe Leu Val Ile Tyr Ile Gln Ser Leu Tyr Thr Arg Asn
145           150           155           160
Leu Arg Tyr Cys Lys Lys Asn Gln Leu Ser His Ser Tyr Cys Leu His
165           170           175
Gln Asp Val Met Lys Leu Ala Cys Ser Asp Asn Arg Ile Asp Val Ile
180           185           190
Tyr Gly Phe Phe Gly Ala Leu Cys Leu Met Val Asp Phe Ile Leu Ile
195           200           205
Ala Val Ser Tyr Thr Leu Ile Leu Lys Thr Val Leu Gly Ile Ala Ser
210           215           220
Lys Lys Glu Gln Leu Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys
225           230           235           240
Ala Val Ile Ile Phe Tyr Leu Pro Ile Ile Asn Leu Ala Val Val His
245           250           255
Arg Phe Ala Arg His Val Ser Pro Leu Ile Asn Val Leu Met Ala Asn
260           265           270
Val Leu Leu Leu Val Pro Pro Leu Thr Asn Pro Ile Val Tyr Cys Val
275           280           285
Lys Thr Lys Lys Gln Ile Arg Asp Gly Leu Asn Val Lys Leu Thr Arg Lys
290           295           300
Ile Arg Cys Arg Gly Asp
305           310

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&lt;210&gt; 227

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(474)

&lt;400&gt; 227

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atg gaa cca gag aat ggt acg agg att tta gga ttt ctt ctt ctg gga 48
Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
 1           5           10           15

```

258/261

```

ctt tca gag gaa cca gaa ttg cag ccc gtt atg ttt gga ctc ttc ctc   96
Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
                20                25                30

tcc atg tat ctg aca act gtg ttt gga aac ctg ctc atc atc ctg gcc   144
Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
                35                40                45

atc tgc tct ggt tcc cac ctc cac acc ccc atg tac ttc ttc ctc tct   192
Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
                50                55                60

aac ctg tcc ttt gta gac atc tgt gtt acc tcc acc aca gtc cca aag   240
Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
                65                70                75                80

aca ctg tca aac atc cgg aca cag agt aaa gtc atc acc tat gca ggt   288
Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
                85                90                95

tgc atc acc cag atg tac ttt ttt gta ctc ttt ata gtg ttg gac agc   336
Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
                100                105                110

tta ctc ttg acc gtg atg gcc tat gac cag ttt gtg gcc atc tgt cac   384
Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
                115                120                125

ccc ctg cac tac acg gtc atc gtg aac cct cgg ctc tgt gga ctg ctg   432
Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
                130                135                140

gtt ctg gcg tcc tgg atc atg agt gcc ctg aat tcc ttg ata         474
Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile
                145                150                155

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&lt;210&gt; 228

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 228

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Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
 1      5      10      15
Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
 20     25     30
Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
 35     40     45
Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50     55     60
Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
 65     70     75     80
Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
 85     90     95
Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
100    105    110
Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
115    120    125
Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
130    135    140

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259/261

Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile  
 145 150 155

<210> 229  
 <211> 873  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(873)

<400> 229  
 tct cca ttt ata ttt tca ggt ctc tta ttt caa ctt ggg ttg ctt cca 48  
 Ser Pro Phe Ile Phe Ser Gly Leu Leu Phe Gln Leu Gly Leu Leu Pro  
 1 5 10 15

ctt ttt ttt ttt ttt ttt ttt ttt ttg aga tgg agt ctc gct ctt 96  
 Leu Phe Phe Phe Phe Phe Phe Phe Leu Arg Trp Ser Leu Ala Leu  
 20 25 30

aat tac tta ata atg gga tgt att tgt tgg ttc ctg cac aac ttc tca 144  
 Asn Tyr Leu Ile Met Gly Cys Ile Cys Trp Phe Leu His Asn Phe Ser  
 35 40 45

aat gta gga atc aga cta gac tgt gtc acc ctg atg cca agg ctg ctc 192  
 Asn Val Gly Ile Arg Leu Asp Cys Val Thr Leu Met Pro Arg Leu Leu  
 50 55 60

ttt agt cta gta ggg ccc act tgt cac att tcc ttt ttg gag ggt tgt 240  
 Phe Ser Leu Val Gly Pro Thr Cys His Ile Ser Phe Leu Glu Gly Cys  
 65 70 75 80

gct agg cag tgg ttt tat ttc ttt ttt att atg ggt caa ctt gat tct 288  
 Ala Arg Gln Trp Phe Tyr Phe Phe Phe Ile Met Gly Gln Leu Asp Ser  
 85 90 95

ttt tta tta tta tta tac ttt aat ttc tta ata agt tct cat ttg ttt 336  
 Phe Leu Leu Leu Leu Tyr Phe Asn Phe Leu Ile Ser Ser His Leu Phe  
 100 105 110

att ctg atg gtc ttc att tgt aat tgt atg tcc att gcc tgt atg agt 384  
 Ile Leu Met Val Phe Ile Cys Asn Cys Met Ser Ile Ala Cys Met Ser  
 115 120 125

ttg caa aaa ctt cta aca ata tca cct tta tta cta agt ttt tgt ttg 432  
 Leu Gln Lys Leu Leu Thr Ile Ser Pro Leu Leu Leu Ser Phe Cys Leu  
 130 135 140

gaa aat ata att att agg cat ttt ctt tgt gaa agt gtg cca ctt ctc 480  
 Glu Asn Ile Ile Ile Arg His Phe Leu Cys Glu Ser Val Pro Leu Leu  
 145 150 155 160

ctg ttc ctt tct tgc tct gtc acc agg ctg gaa gag cta atg ttg agt 528  
 Leu Phe Leu Ser Cys Ser Val Thr Arg Leu Glu Glu Leu Met Leu Ser  
 165 170 175

ctg aca gcc agt ggc tgt gtc atc atg atc tgc ttt gcc ctc act gtc 576  
 Leu Thr Ala Ser Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val  
 180 185 190

260/261

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ctc tct tac atc cgc atc ttg gcc aca gtg gtt cag atc cgt tca gca 624
Leu Ser Tyr Ile Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala
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gcc agc cgc cgg aag gcc ttc tcc acc tgt tct tcc cac ctg ggc atg 672
Ala Ser Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His Leu Gly Met
      210                215                220

gtg ctc ctg ttc tat gcc acc ggc agc tcc acc tac atg cga ccc acc 720
Val Leu Leu Phe Tyr Gly Thr Gly Ser Ser Thr Tyr Met Arg Pro Thr
      225                230                235                240

acc cgc tac tcc ccg ctg gaa ggg cgc ttg gct gct gtc ttc tac tcc 768
Thr Arg Tyr Ser Pro Leu Glu Gly Arg Leu Ala Ala Val Phe Tyr Ser
      245                250                255

atc ctc ata ccc acc ctg aat ccg ctc atc tac agc ctg agg aac cag 816
Ile Leu Ile Pro Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln
      260                265                270

gac atg aag aga gcc ctg tgg aag ctc tat ctc cag tct cac tct cac 864
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Ser Gly Trp
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<210> 230  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

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Leu Phe Phe Phe Phe Phe Phe Phe Phe Leu Arg Trp Ser Leu Ala Leu
      20          25          30
Asn Tyr Leu Ile Met Gly Cys Ile Cys Trp Phe Leu His Asn Phe Ser
      35          40          45
Asn Val Gly Ile Arg Leu Asp Cys Val Thr Leu Met Pro Arg Leu Leu
      50          55          60
Phe Ser Leu Val Gly Pro Thr Cys His Ile Ser Phe Leu Glu Gly Cys
      65          70          75          80
Ala Arg Gln Trp Phe Tyr Phe Phe Phe Ile Met Gly Gln Leu Asp Ser
      85          90          95
Phe Leu Leu Leu Leu Tyr Phe Asn Phe Leu Ile Ser Ser His Leu Phe
      100         105         110
Ile Leu Met Val Phe Ile Cys Asn Cys Met Ser Ile Ala Cys Met Ser
      115         120         125
Leu Gln Lys Leu Leu Thr Ile Ser Pro Leu Leu Leu Ser Phe Cys Leu
      130         135         140
Glu Asn Ile Ile Ile Arg His Phe Leu Cys Glu Ser Val Pro Leu Leu
      145         150         155         160
Leu Phe Leu Ser Cys Ser Val Thr Arg Leu Glu Glu Leu Met Leu Ser
      165         170         175
Leu Thr Ala Ser Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val
      180         185         190
Leu Ser Tyr Ile Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala
      195         200         205

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261/261

Ala	Ser	Arg	Arg	Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Gly	Met
210						215						220			
Val	Leu	Leu	Phe	Tyr	Gly	Thr	Gly	Ser	Ser	Thr	Tyr	Met	Arg	Pro	Thr
225					230					235					240
Thr	Arg	Tyr	Ser	Pro	Leu	Glu	Gly	Arg	Leu	Ala	Ala	Val	Phe	Tyr	Ser
				245					250						255
Ile	Leu	Ile	Pro	Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Gln
			260					265						270	
Asp	Met	Lys	Arg	Ala	Leu	Trp	Lys	Leu	Tyr	Leu	Gln	Ser	His	Ser	His
		275					280					285			
Ser	Gly	Trp													
290															

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A61K 45/00, 39/00

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Published:

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(54) Title: NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

# INTERNATIONAL SEARCH REPORT

Intern..... Application No  
PCT/IB 02/02481

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N5/10 C07K14/705 C07K16/40 C12Q1/68  
G01N33/50 A61K45/00 A61K39/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, BIOSIS, SEQUENCE SEARCH, EMBL

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 27158 A (FUCHS TANIA ;GLUSMAN GUSTAVO (IL); LANCET DORON (IL); YEDA RES & D) 19 April 2001 (2001-04-19) SEQ ID NO: 691 & 1623 ---	1-52
X	DATABASE EMBL20 June 2000 (2000-06-20) SYCAMORE N: "Human DNA sequence from clone RP11-542K23 on chromosome 9" Database accession no. AL359636 XP002231347 Positions 138690 - 139610 --- -/--	1-52

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

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Date of the actual completion of the international search

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Authorized officer

Bucka, A

# INTERNATIONAL SEARCH REPORT

Inter...al Application No  
PCT/IB 02/02481

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL10 March 1998 (1998-03-10) GIORGI D G; ROUQUIER S P: "Homo sapiens olfactory receptor (OR1-26) gene, partial cds." Database accession no. U86216 XP002231348 the whole document	1-52
X	-& ROUQUIER S ET AL.: "Distribution of olfactory receptor genes in the human genome" NATURE GENETICS, NEW YORK, NY, US, vol. 18, no. 3, March 1998 (1998-03), pages 243-250, XP002111208 ISSN: 1061-4036 the whole document	1-52
P,X	WO 01 68805 A (SENOYX INC) 20 September 2001 (2001-09-20) * AOLFR250 sequences * page 189	1-52
P,X	WO 01 90359 A (INCYTE GENOMICS INC ;KALLICK DEBORAH A (US); PATTERSON CHANDRA (US) 29 November 2001 (2001-11-29) SEQ ID NO: 7 & 30	1-52
P,X	WO 02 06345 A (ALSOBROOK JOHN P II ;BURGESS CATHERINE E (US); MACDOUGALL JOHN R ( ) 24 January 2002 (2002-01-24) SEQ ID NO: 13 & 14 page 26 -page 33	1-52
X	DATABASE EMBL25 April 2000 (2000-04-25) YASUOKA ET AL.: "Rattus norvegicus gust43 gene for gustatory receptor 43, complete cds." Database accession no. AB038167 XP002231349 the whole document	1-52
A	ABE K ET AL: "PRIMARY STRUCTURE AND CELL-TYPE SPECIFIC EXPRESSION OF A GUSTATORY G PROTEIN-COUPLED RECEPTOR RELATED TO OLFACTORY RECEPTORS" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 268, no. 16, 5 June 1993 (1993-06-05), pages 12033-12039, XP000857320 ISSN: 0021-9258 the whole document	1-52

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

# INTERNATIONAL SEARCH REPORT

Inter... Application No  
PCT/IB 02/02481

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL9 April 1996 (1996-04-09) THOMAS M B: "Rattus norvegicus taste bud receptor protein TB 334 (TB 334) gene, complete cds." Database accession no. U50947 XP002231350 the whole document</p>	1-52
X	<p>-&amp; THOMAS M B ET AL.: "Chemoreceptors expressed in taste, olfactory and male reproductive tissues" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, ELSEVIER SCIENCE PUBLISHERS, BARKING, GB, vol. 178, no. 1, 31 October 1996 (1996-10-31), pages 1-5, XP004043330 ISSN: 0378-1119 the whole document</p>	1-52
X	<p>--- DATABASE EMBL21 October 1999 (1999-10-21) SHARON D ET AL.: "Gorilla gorilla isolate PPOR1P1 olfactory receptor gene, partial cds." Database accession no. AF101763 XP002231351 the whole document -&amp; SHARON DROR ET AL.: "Primate evolution of an olfactory receptor cluster: Diversification by gene conversion and recent emergence of pseudogenes" GENOMICS, ACADEMIC PRESS, SAN DIEGO, US, vol. 61, no. 1, 1 October 1999 (1999-10-01), pages 24-36, XP002180154 ISSN: 0888-7543 the whole document</p>	1-52
A	<p>--- FUCHS TANIA ET AL: "The human olfactory subgenome: From sequence to structure and evolution" HUMAN GENETICS, BERLIN, DE, vol. 108, no. 1, January 2001 (2001-01), pages 1-13, XP002178958 the whole document --- -/--</p>	1-52

# INTERNATIONAL SEARCH REPORT

Intern. Application No  
PCT/IB 02/02481

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>TRASK B J ET AL: "Members of the olfactory receptor gene family are contained in large blocks of DNA duplicated polymorphically near the ends of human chromosomes"</p> <p>HUMAN MOLECULAR GENETICS, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 7, no. 1, January 1998 (1998-01), pages 13-26, XP002135641</p> <p>ISSN: 0964-6906</p> <p>the whole document</p> <p>-----</p>	1-52



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 02/02481

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Although claims 31 and 37 to 39 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-52 (all partially and insofar as applicable)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## Continuation of Box I.2

Present claims 18 to 24, 26, 29 to 31, 33, 34 and 37 to 39 relate to compounds ("an agent") defined by reference to a desirable characteristic or property, namely their property to alter the activity of the claimed protein or to influence its expression.

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to antibodies and ribozymes, as referred to in claims 18 and 23, and antisense nucleic acids, as mentioned in claim 30.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-52,  
all partially and insofar as applicable

an isolated olfactory G protein-coupled receptor having the amino acid sequence SEQ ID NO: 2, isolated nucleic acids encoding said protein, represented by SEQ ID NO:1, vectors and host cells containing these nucleic acids, methods for the identification of modulators of said protein and methods for the detection of said protein or the nucleic acids encoding it

Inventions 2 to 115: claims 1-52,  
all partially and insofar as applicable

an isolated olfactory G protein-coupled receptor, isolated nucleic acids encoding said protein, vectors and host cells containing these nucleic acids, methods for the identification of modulators of said protein and methods for the detection of said protein or the nucleic acids encoding it,

wherein each separate invention is represented by an odd numbered polynucleotide sequence comprising SEQ ID NO: 3 to 229 and an even numbered protein sequence comprising SEQ ID NO: 4 to 230,

wherein invention 2 is represented by SEQ ID NO: 3 and 4, invention 3 is represented by SEQ ID NO: 5 and 6, continuing to invention 115, represented by SEQ ID NO: 229 and 230

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 02/02481

Patent document cited in search report		Publication date		Patent family member(s)		Publication date
WO 0127158	A	19-04-2001	AU	1326201 A		13-02-2001
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			WO	0206345 A2		24-01-2002
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